SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: Maertens, Geert Bosman, Fons De Martynoff, Guy Buyse, Marie-Ange
 - (ii) TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.
 - (iii) NUMBER OF SEQUENCES: 122
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: NIXON & VANDERHYE
 - (B) STREET: 1100 North Glebe Road, 8th Floor
 - (C) CITY: Arlington, VA 22201
 - (E) COUNTRY: USA
 - (F) ZIP: 22201
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: Unassigned
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Sadoff, B. J.
 - (B) REGISTRATION NUMBER: 36663
 - (C) REFERENCE/DOCKET NUMBER: 2551-61
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703) 816-4000
 - (B) TELEFAX: (703) 816-4100
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
GGCATGCAAG CTTAATTAAT T	21
(2) INFORMATION FOR SEQ ID NO: 2:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 68 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
CCGGGGAGGC CTGCACGTGA TCGAGGGCAG ACACCATCAC CACCATCACT AATAGTTAAT	60
TAACTGCA	68
(2) INFORMATION FOR SEQ ID NO: 3:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 642 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1639	
<pre>(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 1636</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA CTG TCC TGT Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys 1 5 10 15	48
CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG TCC GGG ATG Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met 20 25 30	96
TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	144

		35					40					45					
GCG G Ala A	GAC Asp 50	ATG Met	ATC Ile	ATG Met	CAC His	ACC Thr 55	CCC Pro	GGG Gly	TGC Cys	GTG Val	CCC Pro 60	TGC Cys	GTT Val	CGG Arg	GAG Glu		192
AAC A Asn A 65																	240
AGG A																	288
CTC C																	336
TGC C	GGA Gly	TCT Ser 115	GTC Val	TTC Phe	CTC Leu	GTC Val	TCC Ser 120	CAG Gln	CTG Leu	TTC Phe	ACC Thr	ATC Ile 125	TCG Ser	CCT Pro	CGC Arg		384
CGG (432
ATA A Ile 7 145																	480
ACA A	ACG Thr	GCC Ala	CTG Leu	GTG Val 165	GTA Val	TCG Ser	CAG Gln	CTG Leu	CTC Leu 170	CGG Arg	ATC Ile	CCA Pro	CAA Gln	GCT Ala 175	GTC Val	,	528
GTG (Leu			576
TAC TYT																	624
CTC C				TAA	TAG												642

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 212 amino acids
 - (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys

Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met

15

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20 25	31
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Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala 35 40 45

Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu 50 60

Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala 65 70 75 80

Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu 85 90 95

Leu Val Gly Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu 100 105 110

Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg 115 120 125

Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His 130 135 140

Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro 145 150 155 160

Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val 165 170 175

Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala 180 185 190

Tyr Tyr Ser Met Val Gly Asn Tro Ala Lys Val Leu Ile Val Met Leu 195 200 205

Leu Phe Ala Leu 210

- (2) INFORMATION FOR SEQ ID NO: 5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..792

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

	(,															
					ATC Ile											48
					CTC Leu											96
					GTC Val											144
					GGT Gly											192
					GTT Val 70											240
					GTC Val											288
					ATG Mec											336
					TCT Ser											384
					GCC Ala											432
					GGG Gly 150											480
					TCT Ser											528
				CAT	GAG Glu				GAC					ATC		576
					GGT Gly											624
					GCC Ala										CCA Pro	672
					ATG Met 230											720
GGT	CTC	GCC	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	768

Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile 245 250 255

GTG ATG CTA CTC TTT GCT CCC TAATAG Val Met Leu Leu Phe Ala Pro 260 795

- (2) INFORMATION FOR SEQ ID NO: 6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 263 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu 1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val 85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His 130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val 145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile 165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr 180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn 195 200 205

Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro 210 215 220

Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala

Gly	Leu	Ala	Tyr	Tyr 245	Ser	Mec	Val	Gly	Asn 250	Trp	Ala	Lys	Val	Leu 255	Ile	
Val	Met	Leu	Leu 260	Phe	Ala	Pro										
(2)	INFO	RMAT	CION	FOR	SEQ	ID N	10: 7	7:								
	(i)	(P (C	QUENC A) LE B) TY C) ST D) TO	ENGTI PE: PANI	i: 63 nucl	3 ba .eic ESS:	ase s acid	pairs 1	5							
	(ii)	MOI	LECUI	LE TY	PE:	CDNA	Ŧ									
	(iii)	HYP	POTHE	ETIC	AL: 3	10										
	(iii)	ANT	TI-SE	ENSE:	NO											
	(ix)	(2	ATURS A) NZ B) L(AME/E			530			٠						
	(ix)	(2	ATURE A) NZ B) LO	AME/				ide								
										_						
			QUENC					-								4.0
	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CIT	ACG	TGC	GGC	TTC Phe				48
Met 1 ATG	TTG Leu GGG	GGT Gly TAC	AAG Lys ATT	GTC Val 5	ATC Ile	GAT Asp GTC	ACC Thr GGC	CTT Leu GCC	ACG Thr 10	TGC Cys CTA	GGC Gly GGG		Ala	Asp 15 GCC	Leu AGA	48 96
Met 1 ATG Met	TTG Leu GGG Gly	GGT Gly TAC Tyr	AAG Lys ATT Ile 20	GTC Val 5 CCG Pro	ATC Ile CTC Leu GTC	GAT Asp GTC Val	ACC Thr GGC GLy GTT	CTT Leu GCC Ala 25	ACG Thr 10 CCC Pro	TGC Cys CTA Leu GAC	GGC Gly GGG Gly	Phe GGT	GCT Ala 30	Asp 15 GCC Ala TAT	Leu AGA Arg GCA	
Met 1 ATG Met GCC Ala	TTG Leu GGG Gly CTG Leu	GGT Gly TAC Tyr GCG Ala 35	AAG Lys ATT Ile 20 CAT His	GTC Val 5 CCG Pro GGC Gly	ATC Ile CTC Leu GTC Val	GAT Asp GTC Val CGG Arg	ACC Thr GGC Gly GTT Val 40 TCT	CTT Leu GCC Ala 25 CTG Leu	ACG Thr 10 CCC Pro GAA Glu	TGC Cys CTA Leu GAC Asp	GGC Gly GGG Gly GGC Gly	GGT Gly	GCT Ala 30 AAC Asn	Asp 15 GCC Ala TAT TYT	AGA Arg GCA Ala	96
Met 1 ATG Met GCC Ala ACA Thr	TTG Leu GGG Gly CTG Leu GGG Gly 50	GGT Gly TAC Tyr GCG Ala 35 AAT Asn	AAG Lys ATT Ile 20 CAT His TTG Leu CTG	GTC Val 5 CCG Pro GGC Gly CCT Pro	ATC Ile CTC Leu GTC Val GGT Gly ATT	GAT Asp GTC Val CGG Arg TGC Cys 55	ACC Thr GGC Gly GTT Val 40 TCT Ser	CTT Leu GCC Ala 25 CTG Leu TTC Phe	ACG Thr 10 CCC Pro GAA Glu TCT Ser	TGC Cys CTA Leu GAC Asp ATC Ile	GGC Gly GGG Gly GGC Gly TTC Phe 60 GAG	Phe GGT Gly GTG Val 45 CTC	GCT Ala 30 AAC Asn TTG Leu	Asp 15 GCC Ala TAT Tyr GCT Ala	AGA Arg GCA Ala TTA Leu	96 144
Met 1 ATG Met GCC Ala ACA Thr CTG Leu 65	TTG Leu GGG Gly CTG Leu GGG Gly 50 TCC Ser	GGT Gly TAC Tyr GCG Ala 35 AAT Asn TGT Cys	AAG Lys ATT Ile 20 CAT His TTG Leu CTG Leu TAC	GTC Val 5 CCG Pro GGC Gly CCT Pro ACC Thr	ATC Ile CTC Leu GTC Val GGT Gly ATT Ile 70 GTC	GAT Asp GTC Val CGG Arg TGC Cys 55 CCA Pro	ACC Thr GGC Gly GTT Val 40 TCT Ser GCT Ala	CTT Leu GCC Ala 25 CTG Leu TTC Phe TCC Ser	ACG Thr 10 CCC Pro GAA Glu TCT Ser GCT Ala	TGC Cys CTA Leu GAC Asp ATC Ile TAT Tys 75	GGC Gly GGG Gly TTC Phe 60 GAG Glu	GGT Gly GTG Val 45 CTC Leu GTG	GCT Ala 30 AAC Asn TTG Leu CGC Arg	Asp 15 GCC Ala TAT Tyr GCT Ala AAC Asn	AGA Arg GCA Ala TTA Leu GTG Val 80	96 144 192

				TCT Ser					ACG Thr	384
				GCC Ala						432
				GGG Gly 150						480
				TCT Ser						528
				GAG Glu					TAT Tyr	576
				GGT Gly						624
TGG Trp	TAAT	AG								633
٠ي	210									

- (2) INFORMATION FOR SEQ ID NO: 8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 amino acids

 - (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu

Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 50 55 60

Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Vai Arg Asn Val 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 105

Val	Arg	Glu 115	Asn	Asn	Ser	Ser	Arg 120	Cys	Trp	Val	Ala	Leu 125	Thr	Pro	Thr	
Leu	Ala 130	Ala	Arg	Asn	Ala	Ser 135	Val	Pro	Thr	Thr	Thr 140	Ile	Arg	Arg	His	
Val 145	qeA	Leu	Leu	Val	Gly 150	Ala	Ala	Ala	Phe	Cys 155	Ser	Ala	Met	Tyr	Val 160	
Gly	Asp	Leu	Cys	Gly 165	Ser	Val	Phe	Leu	Val 170	Ser	Gln	Leu	Phe	Thr 175	Ile	
Ser	Pro	Arg	Arg 180	His	Glu	Thr	Val	Gln 185	qeA	Cys	Asn	Cys	Ser 190	Ile	Tyr	
Pro	Gly	His 195	Ile	Thr	Gly	His	Arg 200	Met	Ala	Trp	Asp	Met 205	Met	Met	Asn	
Trp																
(2)	INF	ORMAI	rion	FOR	SEQ	ב פב	10: S	9:								
	(1)	(Z (E	A) LI 3) T C) S	ENGT! (PE: [RAN]	HARAC f: 48 nucl DEDNI DGY:	33 ba Leic ESS:	ase ; acid	pair: i	3							
	(1i)	MOI	LECUI	LE T	YPE:	CDNA	A									
	(iii)	HYI	POTHI	ETIC	AL: 3	10										
	(iii)	ANT	ri-Si	ENSE	: ИО											
	(ix)		A) N2	AME/I	KEY:		480									
	(ix)		4) N	AME/I	KEY: ION:			tiđe								
	(xi	SE	QUEN	CE DI	ESCR:	IPTIO	: NC	SEQ :	ID N	0: 9	:					
					TTC Phe											4.8
					TCC Ser											96
			Thr		GAC Asp			Asn					Tyr		GCA Ala	144

GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu 50

192

 			 TGC Cys 70						24	0
_		_	CCC						28	8
			GCT Ala						33	6
			CTT Leu						38	4
	_	-	CAG Gln						43	2
			ATG Met 150					TAATAG 160	4	83

- (2) INFORMATION FOR SEQ ID NO: 10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys

Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val

Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala

Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu 50 $\,$ 60

Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala 65 70 75 80

Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu

Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu

Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg

Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His

	130	1				135					140)				
Val 145	. Ser	· Gly	' His	Arg	Met 150	Ala	Trp	Asp	Met	Met 155	Met	: Asn	Trp	Ser		
(2)	INF	ORMA	TION	FOR	. SEQ	ID	NO:	11:								
	(i	(A) L B) T C) S	CE C ENGT YPE: TRAN OPOL	H: 4 nuc DEDN	80 b leic ESS:	ase aci sin	pair d	s							
	(ii) MO	LECU	LE T	YPE:	CDN	A									
	(iii) HY	POTH	ETIC	AL:	NO										
	(iii) AN	TI-S	ENSE	: NO											
	(ix	(,		E: AME/ OCAT			477									
	(ix	()	ATUR A) N B) L	E: AME/: OCAT	KEY: ION:	mat	_pep 474	tide								
	(xi) SE	QUEN	CE D	ESCR:	IPTI	ON: :	SEQ :	ID M	D: 1	1:					
ATG Met 1	TCC Ser	GGT Gly	TGC Cys	TCT Ser 5	TTC Phe	TCT Ser	ATC Ile	TTC Phe	CTC Leu 10	TTG Leu	GCC Ala	CTG Leu	CTG Leu	TCC Ser 15	TGT Cys	48
CTG Leu	ACC Thr	ATA Ile	CCA Pro 20	GCT Ala	TCC Ser	GCT Ala	TAT Tyr	GAA Glư 25	GTG Val	CGC Arg	AAC Asn	GTG Val	TCC Ser 30	GGG GLY	GTG Val	96
TAC Tyr	CAT His	GTC Val 35	ACG Thr	AAC Asn	GAC Asp	TGC Cys	TCC Ser 40	AAC Asn	TCA Ser	AGC Ser	ATA Ile	GTG Val 45	TAT Tyr	GAG Glu	GCA Ala	144
GCG Ala	GAC Asp 50	ATG Met	ATC Ile	ATG Met	CAC His	ACC Thr 55	CCC Pro	GGG Gly	TGC Cys	GTG Val	CCC Pro 60	TGC Cys	GTT Val	CGG Arg	GAG Glu	192
GGC Gly 65	AAC Asn	TCC Ser	TCC Ser	CGT Arg	TGC Cys 70	TGG Trp	GTG Val	GCG Ala	CTC Leu	ACT Thr 75	CCC Pro	ACG Thr	CTC Leu	GCG Ala	GCC Ala 80	240
AGG Arg	AAC Asn	GCC Ala	AGC Ser	GTC Val 85	CCC Pro	ACA Thr	ACG Thr	ACA Thr	ATA Ile 90	CGA Arg	CGC Arg	CAC His	GTC Val	GAT Asp 95	TTG Leu	288
CTC	GTT Val	GGG G1v	GCT	GCT	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	336

Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu

TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC

Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg

115	120	125
	140	127

CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT

Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His

130 135 140

GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG

Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp

150

155

- (2) INFORMATION FOR SEQ ID NO: 12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ser Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys
1 10 15

Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val 20 25 30

Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala 35 40 45

Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu
50 60

Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala 65 70 75 80

Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu 85 90 95

Leu Val Gly Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu 100 105 110

Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg 115 120 125

Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His 130 135 140

Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp 145 150 155

- (2) INFORMATION FOR SEQ ID NO: 13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..633

(ix) FEATURE:

(A) NAME/KEY: mat_peptide (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG Met 1	CTG Leu	GGT Gly	AAG Lys	GCC Ala 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACG Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
GTG Val	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96
GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAA Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
ACA Thr	GGG Gly 50	AAT Asn	TTG Leu	CCT Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTA Leu	192
CTG Leu 65	TCC Ser	TGT Cys	CTA Leu	ACC Thr	ATT Ile 70	CCA	GCT Ala	TCC Ser	GCT Ala	TAC Tyr 75	GAG Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240
TCC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288
TAT Tyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
CTC Leu	GCG Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	ATC Ile	CCC Pro	ACT Thr	ACA Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432
GTC Val 145	GAT Asp	TTG Leu	CTC Leu	GTT Val	GGG G1y 150	GCG Ala	GCT Ala	GCT Ala	TTC Phe	TGT Cys 155	TCC Ser	GCT Ala	ATG Met	TAC Tyr	GTG Val 160	480
GGG Gly	GAT Asp	CTC Leu	TGC Cys	GGA Gly 165	TCT Ser	GTC Val	TTC Phe	CTC Leu	GTC Val 170	TCC Ser	CAG Gln	CTG Leu	TTC Phe	ACC Thr 175	ATC Ile	528
TCG Ser	CCT Pro	CGC Arg	CGG Arg	CAT His	GAG Glu	ACG Thr	GTG Val	CAG Gln	GAC Asp	TGC Cys	AAT Asn	TGC Cys	TCA Ser	ATC Ile	TAT Tyr	576

			180					185					190				
CCC Pro	GGC Gly	CAC His 195	ATA Ile	ACG Thr	GGT Gly	CAC His	CGT Arg 200	ATG Mer	GCT Ala	TGG	GAT Asp	ATG Met 205	ATG Met	ATG Met	AAC Asn		624
	TAC Tyr 210	TAA'	TAG														640
(2)	INF	ORMA	rion	FOR	SEQ	ID :	NO: .	14:									
		(1	SEQUI A) LI B) TI	ENGTI YPE :	H: 21	10 ar	mino cid										
			LECUI														
	(xi)	SE(QUENC	CE D	ESCRI	1971(ON: S	SEQ :	ID NO	D: 14	1:						
Met 1	Leu	Gly	Lys	Ala 5	Ile	gzA	Thr	Leu	Thr 10	Cys	Gly	Phe	Ala	Asp 15	Leu		
Val	Gly	Tyr	Ile 20	Pro	Leu	7al	Gly	Ala 25	Pro	Leu	Gly	Gly	Ala 30	Ala	Arg		
Ala	Leu	Ala 35	His	Gly	Val	Arg	Val 40	Leu	Glu	Asp	Gly	Val 45	Asn	Tyr	Ala		
Thr	Gly 50	Asn	Leu	Pro	Gly	Cys 55	Ser	Phe	Ser	Ile	Phe 60	Leu	Leu	Ala	Leu		
Leu 65	Ser	Cys	Leu	Thr	Ile 70	Pro	Ala	Ser	Ala	Tyr 75	Glu	Val	Arg	Asn	Val 80		
Ser	Gly	Met	Tyr	His 85	Val	Thr	Asn	Asp	Cys 90	Ser	Asn	Ser	Ser	I1e 95	Val		
Tyr	Glu	Ala	Ala 100	Asp	Met	Ile	Met	His 105	Thr	Pro	Gly	Cys	Val 110	Pro	Cys	***	
Val	Arg	Glu 115	Asn	Asn	Ser	Ser	Arg 120	Cys	Trp	Val	Ala	Leu 125	Thr	Pro	Thr		
Leu	Ala 130	Ala	Arg	Asn	Ala	Ser 135	Ile	Pro	Thr	Thr	Thr 140	Ile	Arg	Arg	His		
Val 145	qzA	Leu	Leu	Val	Gly 150	Ala	Ala	Ala	Phe	Cys 155	Ser	Ala	Met	Tyr	Val 160		
Gly	qzA	Leu	Cys	Gly 165	Ser	Val	Phe	Leu	Va1 170	Ser	Gln	Leu	Phe	Thr 175	Ile		
Ser	Pro	Arg	Arg 180	His	Glu	Thr	Val	Gln 185	Asp	Cys	Asn	Cys	Ser 190	Ile	Tyr		

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn 195 200 205

26

26

```
Trp Tyr
     210
(2) INFORMATION FOR SEQ ID NC: 15:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 26 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA
   (iii) HYPOTHETICAL: NO
   (iii) ANTI-SENSE: NO
    (xì) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
ATGCCCGGTT GCTCTTTCTC TATCTT
(2) INFORMATION FOR SEQ ID NO: 16:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 26 base pairs
          (B) TYPE: nucleic acid (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: cDNA
   (iii) HYPOTHETICAL: NO
   (iii) ANTI-SENSE: NO
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
ATGTTGGGTA AGGTCATCGA TACCCT
(2) INFORMATION FOR SEQ ID NO: 17:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 30 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: YES

CTATTAGGAC CAGTTCATCA TCATATCCCA	30
(2) INFORMATION FOR SEQ ID NO: 18:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: YES	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:	27
(2) INFORMATION FOR SEQ ID NO: 19:	4:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
ATACGACGCC ACGTCGATTC CCAGCTGTTC ACCATC	36
(2) INFORMATION FOR SEQ ID NO: 20:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: CDNA	
(iii) HYPOTHETICAL: NO (iii) ANTI-SENSE: YES	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:	
GATGGTGAAC AGCTGGGAAT CGACGTGGCG TCGTAT	36
(2) INFORMATION FOR SEQ ID NO: 21:	

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 723 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS (B) LOCATION: 1..720
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide (B) LOCATION: 1..717
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

	ATG Met 1	TTG Leu	GGT Gly	AAG Lys	GTC Val 5	ATC Ile	GAT Asp	ACC Thr	CTT	ACA Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48	
	GTG Val	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	3CC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96	
	GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144	
	ACA Thr	GGG Gly 50	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTG Leu	192	
	CTG Leu 65	TCC Ser	TGT Cys	CTG Leu	ACC Thr	GTT Val 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr 75	GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240	
	TCC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288	
	TAT Tyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336	
	GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384	
	Leu	130	Ата	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	CGA Arg	Arg	His	132	
,	GTC Val	GAT Asp	TCC Ser	CAG Gln	CTG Leu	TTC Phe	ACC Thr	ATC Ile	TCG Ser	CCT Pro	CGC Arg	CGG	CAT His	GAG Glu	ACG Thr	GTG Val	480	

145					150					155					160	
CAG Gln	GAC Asp	TGC Cys	AAT Asn	TGC Cys 165	TCA Ser	ATC Ile	TAT Tyr	CCC	GGC GLY 170	CAC His	ATA Ile	ACG Thr	GGT Gly	CAC His 175	CGT Arg	528
ATG Met	GCT Ala	TGG Trp	GAT Asp 180	ATG Met	ATG Met	ATG Met	AAC Asn	TGG Trp 185	TCG Ser	CCT	ACA Thr	ACG Thr	GCC Ala 190	CTG Leu	GTG Val	576
GTA Val	TCG Ser	CAG Gln 195	CTG Leu	CTC Leu	CGG Arg	ATC Ile	CCA Pro 200	CAA Gln	GCT Ala	GTC Val	GTG Val	GAC Asp 205	ATG Met	GTG Val	GCG Ala	624
GGG Gly	GCC Ala 210	CAT His	TGG Trp	GGA Gly	GTC Val	CTG Leu 215	GCG Ala	GGT Gly	CTC Leu	GCC Ala	TAC Tyr 220	TAT Tyr	TCC Ser	ATG Met	GTG Val	672
GGG Gly 225	AAC Asn	TGG Trp	GCT Ala	AAG Lys	GTT Val 230	TTG Leu	ATT Ile	GTG Val	ATG Met	CTA Leu 235	CTC Leu	TTT Phe	GCT Ala	CCC Pro	TAATAG 240	723

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu 1 5 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 50 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His 130 135 140

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val

145					150					155					160	
Gln	qzƙ	Cys	Asn	Cys 165	Ser	Ile	Tyr	Pro	Gly 170		Ile	Thr	Gly	His 175	Arg	
Met	Ala	Trp	Asp 180	Met	Met	Mec	Asn	Trp 185	Ser	Pro	Thr	Thr	Ala 190	Leu	Val	
Val	Ser	Gln 195	Leu	Leu	Arg	Ile	Pro 200	Gln	Ala	Val	Val	Asp 205	Met	Val	Ala	
Gly	Ala 210	His	Trp	Gly	Val	Leu 215	Ala	Gly	Leu	Ala	Tyr 220	Tyr	Ser	Met	Val	
Gly 225	Asn	Trp	Ala	Lys	Val 230	Leu	Ile	Val	Met	Leu 235	Leu	Phe	Ala	Pro		
((ii) (iii) (iii) (ix)	SEQ (I (I) (I) MOI HY! ANT: (I) (I) (I)	QUENCA) LH B) TY C) ST C) ST C) TO LECUI POTHE ATURE A) NA B) LO ATURE A) NA B) LO	CE CIENGTI (PE: (PRANI) (POLCE ETICA ETICA ENSE E: (AME/I (CAT)	SEQ HARACH: 50 nuc: DEDNI OGY: YPE: AL: 1 : NO KEY: ION: ESCRI	CTERISION CONTRACTOR C	ISTICAL ACTOR ACT	CS: pairs i jle		D: 23	3:					
ATG Met 1	TTG	GGT	AAG	GTC	ATC Ile	GAT	ACC	CTT	ACA	TGC	GGC	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
GTG Val	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC	AGG Arg	96
GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
ACA Thr	GGG Gly 50	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTG Leu	192
CTG Leu	TCC Ser	TGT Cys	CTG Leu	ACC Thr	GTT Val	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr	GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val	240

65					70					75					80		
TCC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	28	8
TAT Tyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG	TGC Cys	GTG Val 110	BL0 CCC	TGC Cys	33	6
GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC	ACG Thr	38	4
CTC Leu	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	43	2
GTC Val 145	GAT Asp	TCC Ser	CAG Gln	CTG Leu	TTC Phe 150	ACC Thr	ATC Ile	TCG Ser	CCT Pro	CGC Arg 155	CGG Arg	CAT His	GAG Glu	ACG Thr	GTG Val 160	48	0
CAG Gln	GAC Asp	TGC Cys	AAT Asn	TGC Cys 165	TCA Ser	ATC Ile	TAT Tyr	CCC Pro	GGC Gly 170	CAC His	ATA Ile	ACG Thr	GGT Gly	CAC His 175	CGT Arg	52	:8
ATG Met	GCT Ala	TGG Trp	GAT Asp 180	ATG Met	ATG Met	ATG Met	AAC Asn	TGG Trp 185	TAAT	TAG						56	i1
(2)		(i) S (<i>I</i> (E	FION SEQUE (A) LE (B) TO	NCE NGTI	CHAF : 18 amin	ACTS Sam	RIST nino :id	CICS:									
	(ii)	MOI	ECUL	E TY	PE:	prot	ein										
	(xi)	SEC	UENC	E DE	SCRI	PTIC	N: S	EQ I	D NO): 24	:						
Met 1	Leu	Gly	Lys	Val 5	Ile	Asp	Thr	Leu	Thr 10	Cys	Gly	Phe	Ala	Asp 15	Leu		
Val	Gly	Tyr	Ile 20	Pro	Leu	Val	Gly	Ala 25	Pro	Leu	Gly	Gly	Ala 30	Ala	Arg		
Ala	Leu	Ala 35	His	Gly	Val	Arg	Val 40	Leu	Glu	Asp	Gly	Val 45	Asn	Tyr	Ala		
Thr	Gly 50	Asn	Leu	Pro	Gly	Cys 55	Ser	Phe	Ser	Ile	Phe 60	Leu	Leu	Ala	Leu		
Leu 65	Ser	Cys	Leu	Thr	Vál 70	Pro	Ala	Ser	Ala	Tyr 75	Glu	Val	Arg	Asn	Val 80		
Ser	Gly	Met	Tyr	His 85	Val	Thr	Asn	Asp	Cys 90	Ser	Asn	Ser	Ser	Ile 95	Val		

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 100 $\,$ 100 $\,$

Val	Arg	Glu 115	Asn	Asn	Ser	Ser	Arg 120	Cys	Trp	Val	Ala	Leu 125	Thr	Pro	Thr	
Leu	Ala 130	Ala	Arg	Asn	Ala	Ser 135	Val	Pro	Thr	Thr	Thr 140	Ile	Arg	Arg	His	
Val 145	Asp	Ser	Gln	Leu	Phe 150	Thr	Ile	Ser	Pro	Arg 155	Arg	His	Glu	Thr	Val 160	
Gln	qzA	Cys	Asn	Cys 165	Ser	Ile	Tyr	Pro	Gly 170	His	Ile	Thr	Gly	His 175	Arg	
Met	Ala	Trp	Asp 180	Met	Met	Met	Asn	Trp 185								
(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	NO: 2	25 :								
	(i)	() () ()	A) LE 3) TY C) ST	CE CHENGTH PE: TRANI	i: 60 nucl EDNI)6 ba Leic ISS:	ase pació	oairs i	5							
	(ii	MO	LECUI	E T	PE:	CDNA	Ŧ							•		
	(iii)	HY	OTHE	ETICA	L: 1	10										
	(iii)	AN	TI-SE	INSE :	МО											
	(ix)	(2		E: ME/F CATI			503									
	(ix)	(2	ATURE	ME/K	EY:	mat_	_pept	ide								
			-,													
	(xi)	SE						EQ I	D NO): 25	i :					
ATG Met 1	TTG	GGT	QUENC AAG	E DE	SCRI ATC	PTIC	N: S	CTT	ACA	TGC	GGC	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
Met 1 GTG	TTG	GGT Gly TAC	QUENC AAG Lys ATT	GTC Val 5	SCRI ATC Ile CTC	GAT Asp GTC	N: S ACC Thr	CTT Leu GCC	ACA Thr 10	TGC Cys	GGC Gly	Phe	Ala	Asp 15	Leu	4.8 96
GTG Val	TTG Leu GGG	GGT Gly TAC Tyr	QUENC AAG Lys ATT Ile 20 CAT	GTC Val 5 CCG Pro	SCRI ATC Ile CTC Leu GTC	GAT Asp GTC Val	ON: S ACC Thr GGC Gly GTT	CTT Leu GCC Ala 25	ACA Thr 10 CCC Pro	TGC Cys CTA Leu GAC	GGC Gly GGG Gly	Phe GGC Gly	Ala GCT Ala 30	Asp 15 GCC Ala	AGG Arg	
GTG Val GCC Ala	TTG Leu GGG Gly CTG	GGT Gly TAC Tyr GCG Ala 35	QUENC AAG Lys ATT Ile 20 CAT His	GTC Val 5 CCG Pro GGC Gly	SCRI ATC Ile CTC Leu GTC Val	GAT Asp GTC Val CGG Arg	ACC Thr GGC Gly GTT Val 40	CTT Leu GCC Ala 25 CTG Leu	ACA Thr 10 CCC Pro GAG Glu	TGC Cys CTA Leu GAC Asp	GGC Gly GGG Gly TTC	Phe GGC Gly GTG Val 45	GCT Ala 30 AAC Asn	Asp 15 GCC Ala TAT Tyr	Leu AGG Arg GCA Ala	96

TCC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288
TAT Tyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
CTC Leu	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432
GTC Val 145	GAT Asp	TCC Ser	CAG Gln	CTG Leu	TTC Phe 150	ACC Thr	ATC Ile	TCG Ser	CCT Pro	CGC Arg 155	CGG Arg	CAT His	GAG Glu	ACG Thr	GTG Val 160	480
CAG Gln	GAC Asp	TGC Cys	AAT Asn	TGC Cys 165	TCA Ser	ATC Ile	TAT Tyr	CCC Pro	GGC Gly 170	CAC His	ATA Ile	ACG Thr	GGT Gly	CAC His 175	Arg	528
ATG Met	GCT Ala	TGG Trp	GAT Asp 180	ATG Met	ATG Met	ATG Met	AAC Asn	TGG Trp 185	TCG Ser	CCT Pro	ACA Thr	ACG Thr	GCC Ala 190	CTG Leu	GTG Val	576
				CTC Leu				TAAT	TAG							606

- (2) INFORMATION FOR SEQ ID NO: 26:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 200 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu

1 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 50 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val 85 90

Tyr	Glu	Ala	Ala 100	Asp	Met	Ile	Met	His 105	Thr	Pro	Gly	Cys	Val 110	Pro	Cys	
Val	Arg	Glu 115	Asn	Asn	Ser	Ser	Arg 120	Cys	Trp	Val	Ala	Leu 125	Thr	Pro	Thr	
Leu	Ala 130	Ala	Arg	Asn	Ala	Ser 135	Val	Pro	Thr	Thr	Thr 140	Ile	Arg	Arg	His	
Val 145	Asp	Ser	Gln	Leu	Phe 150	Thr	Ile	Ser	Pro	Arg 155	Arg	His	Glu	Thr	Val 160	
Gln	Asp	Cys	Asn	Cys 165	Ser	Ile	Tyr	Pro	Gly 170	His	Ile	Thr	Gly	His 175	Arg	
Met	Ala	Trp	Asp 180	Met	Met	Met	Asn	Trp 185	Ser	Pro	Thr	Thr	Ala 190	Leu	Val	
Val	Ser	Gln 195	Leu	Leu	Arg	Ile	Leu 200									
(2)	INFO	RMAT	rion	FOR	SEQ	ID :	IO: 2	27:								
	(i)	(I (C	A) LE 3) TY C) ST	INGT! PE: RANI	H: 63 nucl	TERI 36 ba leic ESS: line	se p acid	pairs i	5							
	(ii)	MOI	ECUI	E TY	PE:	CDMP	i.									
	(iii)	HYE	OTHE	ETICA	AL: N	10										
	(iii)															
	(ix)	(A	TURE L) NA B) LC	ME/F		CDS 16	:33									
	(ix)	(A	TURE L) NA B) LC	ME/K	ŒY: ION:	mat_ 16	pept 30	ide								
	(xi)	SEÇ	UENC	E DE	SCRI	PTIC	N: S	EQ I	D NO): 27	:					
ATG Met 1	TTG Leu	GGT Gly	AAG Lys	GTC Val 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACA Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
GTG Val	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96
GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
ACA	GGG	AAT	TTG	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	192

Thr	Gly 50	Asn	Leu	Pro	Gly	Cys 55	Ser	Phe	Ser	Ile	Phe 60	Leu	Leu	Ala	Leu	
					GTT Val 70											240
					GTC Val											288
					ATG Met			_		_						336
		-			TCT Ser											384
					GCC Ala											432
					TTC Phe 150											480
					TCA Ser											528
					ATG Met										GTG Val	576
					CGG Arg								His		CAC His	624
	CAC His 210	TAA	TAG													636

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 210 amino acids

 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu 10

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala

35	40	45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 50 55

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val 85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His 130 135 140

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val 145 150 155 160

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg 165 170 175

Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val 180 185 190

Val Ser Gln Leu Leu Arg Ile Val Ile Glu Gly Arg His His His 195 200 205

His His 210

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..627
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..624
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGA TTC GCC GAT CTC ATG

Met 1	Gly	Lys	Val	Ile 5	Asp	Thr	Leu	Thr	Cys 10	Gly	Phe	Ala	qzA	Leu 15	Met	
GGG Gly	TAC Tyr	ATC Ile	CCG Pro 20	CTC Leu	GTC Va1	GGC Gly	GCT Ala	CCC Pro 25	GTA Val	GGA G1y	GGC Gly	GTC Val	GCA Ala 30	AGA Arg	GCC Ala	96
CTT Leu	GCG Ala	CAT His 35	GGC Gly	GTG Val	AGG Arg	GCC Ala	CTT Leu 40	GAA Glu	GAC Asp	GGG Gly	ATA Ile	AAT Asn 45	TTC Phe	GCA Ala	ACA Thr	144
GGG Gly	AAT Asn 50	TTG Leu	CCC Pro	GGT Gly	TGC Cys	TCC Ser 55	TTT Phe	TCT Ser	ATT Ile	TTC Phe	CTT Leu 60	CTC Leu	GCT Ala	CTG Leu	TTC Phe	192
TCT Ser 65	TGC Cys	TTA Leu	ATT Ile	CAT His	CCA Pro 70	GCA Ala	GCT Ala	AGT Ser	CTA Leu	GAG Glu 75	TGG Trp	CGG 'Arg	AAT Asn	ACG Thr	TCT Ser 80	240
GGC Gly	CTC Leu	TAT Tyr	GTC Val	CTT Leu 85	ACC Thr	AAC Asn	GAC Asp	TGT Cys	TCC Ser 90	AAT Asn	AGC Ser	AGT Ser	ATT Ile	GTG Val 95	TAC Tyr	288
GAG Glu	GCC Ala	GAT Asp	GAC Asp 100	GTT Val	ATT Ile	CTG Leu	CAC His	ACA Thr 105	220 CCC	GGC Gly	TGC Cys	ATA Ile	CCT Pro 110	TGT Cys	GTC Val	336
CAG Gln	GAC Asp	GGC Gly 115	AAT Asn	ACA Thr	TCC Ser	ACG Thr	TGC Cys 120	TGG Trp	ACC	CCA Pro	GTG Val	ACA Thr 125	CCT Pro	ACA Thr	GTG Val	384
GCA Ala	GTC Val 130	AAG Lys	TAC Tyr	GTC Val	GGA Gly	GCA Ala 135	ACC Thr	ACC Thr	GCT Ala	TCG Ser	ATA Ile 140	CGC Arg	AGT Ser	CAT His	GTG Val	432
GAC Asp 145	CTA Leu	TTA Leu	GTG Val	GGC Gly	GCG Ala 150	GCC Ala	ACG Thr	ATG Met	TGC Cys	TCT Ser 155	GCG Ala	CTC Leu	TAC Tyr	GTG Val	GGT Gly 160	480
GAC Asp	ATG Met	TGT Cys	GGG Gly	GCT Ala 165	GTC Val	TTC Phe	CTC Leu	GTG Val	GGA Gly 170	CAA Gln	GCC Ala	TTC Phe	ACG Thr	TTC Phe 175	AGA Arg	528
CCT Pro	CGT Arg	CGC Arg	CAT His 180	CAA Gln	ACG Thr	GTC Val	CAG Gln	ACC Thr 185	TGT Cys	AAC Asn	TGC Cys	TCG Ser	CTG Leu 190	TAC Tyr	CCA Pro	576
GGC Gly	CAT His	CTT Leu 195	TCA Ser	GGA G1y	CAT His	CGA Arg	ATG Met 200	GCT Ala	TGG Trp	GAT Asp	ATG Met	ATG Met 205	ATG Met	AAC Asn	TGG Trp	624
TAAT	AG															634

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met 1 10 15

Gly Tyr Ile Pro Leu Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala 20 25 30

Leu Ala His Gly Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr 35 40 45

Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe 50 55 60

Ser Cys Leu Ile His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser 65 70 75 80

Gly Leu Tyr Val Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr 85 90 95

Glu Ala Asp Asp Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val 100 105 110

Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val 115 120 125

Ala Val Lys Tyr Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val 130 135 140

Asp Leu Leu Val Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly 145 150 155 160

Asp Met Cys Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg 165 170 175

Pro Arg Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro 180 185 190

Gly His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp 195 200 205

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- '(ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..627

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

	(X1)	250	OFINC	ב עב	SCAL	PIIV.	14	T 70 T	D 140		•					
ATG Met 1	GGT Gly	AAG Lys	GTC Val	ATC Ile 5	GAT . Asp	ACC Thr	CTA Leu	ACG Thr	TGC Cys 10	GGA Gly	TTC Phe	GCC Ala	GAT Asp	CTC Leu 15	ATG Met	48
GGG Gly	TAT Tyr	ATC Ile	CCG Pro 20	CTC Leu	GTA Val	GGC Gly	GGC Gly	CCC Pro 25	ATT Ile	GGG Gly	GGC Gly	GTC Val	GCA Ala 30	AGG Arg	GCT Ala	96
CTC Leu	GCA Ala	CAC His 35	GGT Gly	GTG Val	AGG Arg	GTC Val	CTT Leu 40	GAG Glu	GAC Asp	GGG Gly	GTA Val	AAC Asn 45	TAT Tyr	GCA Ala	ACA Thr	144
GGG Gly	AAT Asn 50	TTA Leu	CCC Pro	GGT Gly	TGC Cys	TCT Ser 55	TTC Phe	TCT Ser	ATC Ile	TTT Phe	ATT Ile 60	Ten	GCT Ala	CTT Leu	CTC Leu	192
TCG Ser 65	TGT Cys	CTG Leu	ACC Thr	GTT Val	CCG Pro 70	GCC Ala	TCT Ser	GCA Ala	GTT Val	CCC Pro 75	TAC Tyr	CGA Arg	AAT Asn	GCC Ala	TCT Ser 80	240
GGG Gly	ATT Ile	TAT Tyr	CAT His	GTT Val 85	ACC Thr	AAT Asn	GAT Asp	TGC Cys	CCA Pro 90	AAC Asn	TCT Ser	TCC Ser	ATA Ile	GTC Val 95	Tyr	288
GAG Glu	GCA Ala	GAT Asp	AAC Asn 100	CTG Leu	ATC Ile	CTA Leu	CAC His	GCA Ala 105	CCT Pro	GGT Gly	TGC Cys	GTG Val	Pro	Cys	GTC Val	336
ATG Met	ACA Thr	GGT Gly 115	Asn	GTG Val	AGT Ser	AGA Arg	TGC Cys 120	TGG Trp	GTC Val	CAA Gln	ATT	ACC Thr 125	Pro	ACA Thr	CTG Leu	384
TCA Ser	GCC Ala 130	Pro	AGC Ser	CTC Leu	GGA Gly	GCA A1a 135	GTC Val	ACG Thr	GCT Ala	CCT Pro	Leu 140	. Arg	AGA Arg	GCC Ala	GTT Val	432
GAC Ast 145	Tyr	CTA Leu	GCG Ala	GGA Gly	GGG Gly 150	Ala	GCC Ala	CTC Leu	TGC Cys	TCC Ser 155	: Ala	TTA a Lev	A TAC 1 Tyl	GT#	A GGA L Gly 160	480
GAC As <u>r</u>	GCG Ala	TGT Cys	GGG Gly	GCA Ala 165	Leu	TTC Phe	TTG Leu	GTA Val	GGC Gly 170	/ Glr	ATO	G TT(C Phe	C ACC	TA:	r AGG r Arg 5	528
Pro	CGC Arg	CAC Gl:	CAC His 180	Ala	ACG Thr	GTG Val	CAC Glr	AAC 1 Asr 185	Cy:	AA(Asi	TG Cy:	T TC(s Se:	C AT' r Il. 19	е Ту	C AGT r Ser	576
GG(Gl	CAT Y His	GT: Va: 19	l Thi	GGG Gly	C CAC / His	CGG Arg	Met 200	: Ala	A TGO	G GAC p Asi	r ATO	G AT t Me 20	t Me	G AA t As	C TGG n Trp	624

- (2) INFORMATION FOR SEQ ID NO: 32:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
- Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
 1 5 10 15
- Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala 20 25 30
- Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr 35 40 45
- Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 50 55 60
- Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser 65 70 75 80
- Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr 85 90 95
- Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val 100 105 110
- Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu 115 120 125
- Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val 130 135 140
- Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly 145 150 155 160
- Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg 165 170 175
- Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser 180 185 190
- Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp 195 200 205
- (2) INFORMATION FOR SEQ ID NO: 33:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs

	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
	SEQUENCE DESCRIPTION: SEQ ID NO: 33: TGA TGATGAACTG GTC	23
(2) INFO	DRMATION FOR SEQ ID NO: 34:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: CDNA	
(iii)	HYPOTHETICAL: NO	
(iii)) ANTI-SENSE: NO	
CTATTAT) SEQUENCE DESCRIPTION: SEQ ID NO: 34: GGT GGTAAGCCAC AGAGCAGGAG ORMATION FOR SEQ ID NO: 35:) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1476 base pairs	30
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	
(ix	(A) NAME/KEY: CDS (B) LOCATION: 11473	
(ix	(A) NAME/KEY: mat_peptide (B) LOCATION: 11470	
4	i) SEOUENCE DESCRIPTION: SEO ID NO: 35:	

TGG GAT ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG

Trp 1	Asp	Met	Met	Met 5	Asn	Trp	Ser	Pro	Thr 10	Thr	Ala	Leu	Val	Val 15	Ser	
CAG Gln	CTG Leu	CTC Leu	CGG Arg 20	ATC Ile	CCA Pro	CAA Gln	GCT Ala	GTC Val 25	GTG Val	GAC Asp	ATG Met	GTG Val	GCG Ala 30	GGG Gly	GCC Ala	96
CAT His	TGG Trp	GGA Gly 35	GTC Val	CTG Leu	GCG Ala	GGC Gly	CTC Leu 40	GCC Ala	TAC Tyr	TAT Tyr	TCC Ser	ATG Met 45	GTG Val	GGG Gly	AAC Asn	144
TGG Trp	GCT Ala 50	AAG Lys	GTT Val	TTG Leu	GTT Val	GTG Val 55	ATG Met	CTA Leu	CTC Leu	TTT Phe	GCC Ala 60	GGC Gly	GTC Val	GAC Asp	GGG Gly	192
CAT His 65	ACC Thr	Arg	GTG Val	TCA Ser	GGA Gly 70	GGG Gly	GCA Ala	GCA Ala	GCC Ala	TCC Ser 75	GAT Asp	ACC Thr	AGG Arg	GGC GGC	CTT Leu 80	240
			TTT Phe													288
ACC Thr	AAC Asn	GGC Gly	AGT Ser 100	TGG Trp	CAC His	ATC Ile	AAC Asn	AGG Arg 105	ACT Thr	GCC Ala	CTG Leu	AAC Asn	TGC Cys 110	AAC Asn	OAD qaA	336
TCC Ser	CTC Leu	CAA Gln 115	ACA Thr	GGG Gly	TTC Phe	TTT Phe	GCC Ala 120	GCA Ala	CTA Leu	TTC Phe	TAC Tyr	AAA Lys 125	CAC His	AAA Lys	3µe	384
		Ser	GGA Gly													432
AAG Lys 145	Phe	GCT Ala	CAG Gln	GGG Gly	TGG Trp 150	GGT Gly	CCC Pro	CTC	ACT Thr	TAC Tyr 155	ACT Thr	GAG Glu	CCT	AAC Asn	AGC Ser 160	480
TCG Ser	GAC Asp	CAG Gln	AGG Arg	CCC Pro 165	Tyr	TGC Cys	TGG Trp	CAC His	TAC Tyr 170	Ala	CCT	CGA Arg	CCG Pro	TGT Cys 175	GGT Gly	528
				Ser					Pro					The	ST0	576
			. Val					Asr					Pro		TAT	624
		Gly					Asp					Asr			CGG Arg	672
	Pro					Phe					Met				GGG Gly 240	720
					s Gly					Asr					GGC Gly	768

AAC Asn	AAC Asn	ACC Thr	TTG Leu 260	ACC Thr	TGC Cys	CCC	ACT Thr	GAC Asp 265	TGT Cys	TTT Phe	CGG Arg	AAG Lys	CAC His 270	CCC Pro	GAG Glu	816	
GCC Ala	ACC Thr	TAC Tyr 275	GCC Ala	AGA Arg	TGC Cys	GGT Gly	TCT Ser 280	GGG Gly	CCC Pro	TGG Trp	CTG Leu	ACA Thr 285	CCT	AGG Arg	TGT Cys	864	
ATG Met	GTT Val 290	CAT His	TAC Tyr	CCA Pro	TAT Tyr	AGG Arg 295	CTC Leu	TGG Trp	CAC His	TAC Tyr	CCC Pro 300	TGC Cys	ACT Thr	GTC Val	AAC Asn	912	
TTC Phe 305	ACC Thr	ATC Ile	TTC Phe	AAG Lys	GTT Val 310	AGG Arg	ATG Met	TAC Tyr	GTG Val	GGG Gly 315	GGC Gly	GTG Val	GAG Glu	CAC His	AGG Arg 320	960	
TTC Phe	GAA Glu	GCC Ala	GCA Ala	TGC Cys 325	AAT Asn	TGG Trp	ACT Thr	CGA Arg	GGA Gly 330	GAG Glu	CGT Arg	TGT Cys	GAC Asp	TTG Leu 335	GAG Glu	1008	
GAC Asp	AGG Arg	GAT Asp	AGA Arg 340	TCA Ser	GAG Glu	CTT Leu	AGC Ser	CCG Pro 345	CTG Leu	CTG Leu	CTG Leu	TCT Ser	ACA Thr 350	ACA Thr	GAG Glu	1056	
TGG Trp	CAG Gln	ATA Ile 355	CTG Leu	CCC Pro	TGT Cys	TCC Ser	TTC Phe 360	ACC Thr	ACC Thr	CTG Leu	CCG Pro	GCC Ala 365	Leu	TCC Ser	ACC Thr	1104	
GGC Gly	CTG Leu 370	ATC Ile	CAC His	CTC Leu	CAT His	CAG Gln 375	AAC Asn	ATC Ile	GTG Val	GAC Asp	GTG Val 380	CAA Gln	TAC Tyr	CTG Leu	TAC Tyr	1152	
GGT Gly 385	GTA Val	GGG Gly	TCG Ser	GCG Ala	GTT Val 390	GTC Val	TCC Ser	CTT Leu	GTC Val	ATC Ile 395	Lys	TGG Trp	GAG Glu	TAT	GTC Val 400	1200	
CTG Leu	TTG Leu	CTC Leu	TTC Phe	CTT Leu 405	CTC Leu	CTG Leu	GCA Ala	GAC Asp	GCG Ala 410	CGC Arg	ATC Ile	TGC Cys	GCC Ala	TGC Cys 415	TTA Leu	1248	
TGG Trp	ATG Met	ATG Met	CTG Leu 420	CTG Leu	ATA Ile	GCT Ala	CAA Gln	GCT Ala 425	GAG Glu	GCC Ala	GCC Ala	TTA Leu	GAG Glu 430	Asr	CTG Leu	1296	
GTG Val	GTC Val	CTC Leu 435	Asn	GCG Ala	GCG Ala	GCC Ala	GTG Val 440	Ala	GGG Gly	GCG Ala	CAT His	GGC Gly 445	Thr	CTT	TCC Ser	1344	:
TTC Phe	CTT Leu 450	. Val	TTC Phe	TTC Phe	TGT Cys	GCT Ala 455	Ala	TGG Trp	TAC Tyr	ATC	AAG Lys 460	Gl _y	C AGG 7 Arg	CT(GTC 1 Val	1392	•
CCT Pro 465	Gly	GCG	GCA Ala	. TAC . Tyr	GCC Ala 470	. Phe	TAT Tyr	GGC Gly	: GTG Val	TGG Trg 475	Pro	CTO Lev	G CTO	C CTO	G CTT u Leu 480	1440)
			TTA Lev		Pro					ı	STAA					1476	ŝ

- (2) INFORMATION FOR SEQ ID NO: 36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 490 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:
- Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser
- Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala 20 25 30
- His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn 35 40 45
- Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly 50 60
- His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu 65 70 75 80
- Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn 85 90 95
- Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp 100 105 110
- Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe 115 120 125
- Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp 130 135 140
- Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser 145 150 155 160
- Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly 165 170 175
- Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro 180 185 190
- Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr 195 200 205
- Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg 210 215 220
- Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly 225 230 235
- Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly 245 250 255
- Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu 260 265 270
- Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys

: 4

275	280	285
	200	483

Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn 290 295 300

Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg 305 310 315 320

Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu 325 330 335

Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Glu 340 345

Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr 355 360 365

Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr 370 380

Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val 385 390 395 400

Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu 405 410 415

Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu 420 425 430

Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser 435 440 445

Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val 450 455 460

Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu 465 470 480

Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala 485 490

- (2) INFORMATION FOR SEQ ID NO: 37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1021 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: COMA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..1018
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide

(B) LOCATION: 2..1015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

(VI) PROGRACE DESCRIPTION: SEG IN NO: 31:													
G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly 1 5 10 15													
GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys 20 25 30	94												
GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg 35 40 45	142												
GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu 50 60	190												
TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly 65 70 75	238												
AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln 80 95	286												
ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser 100 105 110	334												
GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala 115	382												
CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln 130	430												
AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro 145	478												
GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val 160 175	526												
GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly 180 185 190	574												
GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg 195 200 205	622												
GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys 210 220	670												
ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr	718												

	225					230					235						
TTG Leu 240	ACC Thr	TGC Cys	CCC Pro	ACT Thr	GAC Asp 245	TGT Cys	TTT Phe	CGG Arg	AAG Lys	CAC His 250	CCC Pro	GAG Glu	GCC Ala	ACC Thr	TAC Tyr 255		766
GCC Ala	AGA Arg	TGC Cys	GGT Gly	TCT Ser 260	GGG Gly	CCC Pro	TGG Trp	CTG Leu	ACA Thr 265	CCT Pro	AGG Arg	TGT Cys	ATG Met	GTT Val 270	CAT His		814
TAC Tyr	CCA Pro	TAT Tyr	AGG Arg 275	CTC Leu	TGG Trp	CAC His	TAC Tyr	CCC Pro 280	TGC Cys	ACT Thr	GTC Val	AAC Asn	TTC Phe 285	ACC Thr	ATC Ile		862
TTC Phe	AAG Lys	GTT Val 290	AGG Arg	ATG Met	TAC Tyr	GTG Val	GGG Gly 295	GGC Gly	GTG Val	GAG Glu	CAC His	AGG Arg 300	TTC Phe	GAA Glu	GCC Ala		910
GCA Ala	TGC Cys 305	AAT Asn	TGG Trp	ACT Thr	CGA Arg	GGA Gly 310	GAG Glu	CGT Arg	TGT Cys	GAC Asp	TTG Leu 315	GAG Glu	GAC Asp	AGG Arg	GAT Asp		958
AGA Arg 320	TCA Ser	GAG Glu	CTT Leu	AGC Ser	CCG Pro 325	CTG Leu	CTG Leu	CTG Leu	TCT Ser	ACA Thr 330	ACA Thr	GAG Glu	TGG Trp	CAG Gln	AGT Ser 335	1	1006
	AGA Arg	GCT Ala	TAAT	TA												1	021

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val 1 5 10 15

Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val 20 25 30

Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val 35 40 45

Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe 50 60

Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser 65 70 75 80

Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr
85 90

Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly 100 105 110

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln 115 120 125

Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg 130 135 140

Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala 145 150 155 160

Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val 165 170 175

Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala 180 185 190

Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly 195 200 205

Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr 210 215 220

Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu 225 230 235 240

Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala 245 250 255

Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr 260 265 270

Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe 275 280 285

Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala 290 295 300

Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp 305 310 315 320

Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Glu Trp Gln Ser Gly 325 330 335

Arg Ala

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1034 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..1032

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 2..1029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

(112) Sugumed Bibetti I ION. SEQ ID NO: 39:	
G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly 1 5 10 15	46
GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AP Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Ly 20 25 30	AG 94 ys
GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CG Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Ar 35 40 45	GC 142
GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CT Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Lei Val Ser Le 50 55 50	rC 190 eu
TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GG Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gl 65 70 75	SC 238 Ly
AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CASer Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gl	AA 286 ln 95
ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TC Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Se 100 105 110	CT 334 er
GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GC Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Al 115 120 125	CT 382 La
CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CP Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gl 130	AG 430 In
AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CC Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pr 145	CC 478
GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT G1 Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Va 160 170	al
GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GG Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gl 180 185	GG 574 Ly
GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG Ala Asn Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Ar 195 200	GA 622 rg

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				ACA Thr				-	 		670
				TGC Cys 230							718
				TGT CYs							766
				CCC Pro							814
				CAC His							862
				GTG Val							910
				GGA Gly 310							958
									 	GGG Gly 335	1006
	_		_	TCA Ser	_	AT A	AG				1034

- (2) INFORMATION FOR SEQ ID NO: 40:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val
1 5 10 15

Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val 20 25 30

Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val 35 40 45

Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe 50 60

Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser 65 70 75 80

Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr 85 90 95

Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly 100 105 110

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln 115 120 125

Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg 130 135 140

Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala
145 150 155 160
Ser Gly Val Cys Gly Pro Val Tyr Cys Pho The Pro Car Pro Val

Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val 165 170 175

Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala 180 185 190

Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly 195 200 205

Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr 210 215 220

Cys Gly Gly Pro Pro Cys Asm Ile Gly Gly Ala Gly Asm Asm Thr Leu 225 230 235 240

Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala 245 250 255

Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr 260 265 270

Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe 275 280 285

Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala 290 295 300

Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg 305 310 315

Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Gly Asp Arg Gly Gln 325 330 335

Thr Pro Ser Pro Pro Ser Leu 340

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 945 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..942

(ix) FEATURE:

(A) NAME/KEY: mat_peptide (B) LOCATION: 1..939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATG Met 1	GTG Val	GGG Gly	AAC Asn	TGG Trp 5	GCT Ala	AAG Lys	GTT Val	TTG Leu	GTT Val 10	GTG Val	ATG Met	CTA Leu	CTC Leu	TTT Phe 15	GCC Ala		48
GGC	GTC Val	GAC Asp	GGG Gly 20	CAT His	ACC Thr	CGC Arg	GTG Val	TCA Ser 25	GGA Gly	GGG Gly	GCA Ala	GCA Ala	GCC Ala 30	TCC Ser	GAT Asp		96
ACC Thr	AGG Arg	GGC Gly 35	CTT Leu	GTG Val	TCC Ser	CTC Leu	TTT Phe 40	AGC Ser	CCC Pro	GGG Gly	TCG Ser	GCT Ala 45	CAG Gln	AAA Lys	ATC Ile	1	144
CAG Gln	CTC Leu 50	GTA Val	AAC Asn	ACC Thr	AAC Asn	GGC Gly 55	AGT Ser	TGG Trp	CAC His	ATC Ile	AAC Asn 60	AGG Arg	ACT Thr	GCC Ala	CTG Leu	1	192
AAC Asn 65	TGC Cys	AAC Asn	GAC Asp	TCC Ser	CTC Leu 70	CAA Gln	ACA Thr	GGG Gly	TTC Phe	TTT Phe 75	GCC Ala	GCA Ala	CTA Leu	TTC Phe	TAC Tyr 80	2	240
AAA Lys	CAC His	AAA Lys	TTC Phe	AAC Asn 85	TCG Ser	TCT Ser	GGA Gly	TGC Cys	CCA Pro 90	GAG Glu	CGC Arg	TTG Leu	GCC Ala	AGC Ser 95	TGT Cys	2	288
CGC Arg	TCC Ser	ATC Ile	GAC Asp 100	AAG Lys	TTC Phe	GCT Ala	CAG Gln	GGG Gly 105	TGG Trp	GGT Gly	CCC Pro	CTC Leu	ACT Thr 110	TAC Tyr	ACT Thr	3	336
GAG Glu	CCT Pro	AAC Asn 115	AGC Ser	TCG Ser	GAC Asp	CAG Gln	AGG Arg 120	CCC Pro	TAC Tyr	TGC Cys	TGG Trp	CAC His 125	TAC Tyr	GCG Ala	CCT Pro	3	384
CGA Arg	CCG Pro 130	TGT Cys	GGT Gly	ATT Ile	GTA Val	CCC Pro 135	GCG Ala	TCT Ser	CAG Gln	GTG Val	TGC Cys 140	GGT Gly	CCA Pro	GTG Val	TAT Tyr	4	132
TGC Cys 145	TTC Phe	ACC Thr	CCG Pro	AGC Ser	CCT Pro 150	GTT Val	GTG Val	GTG Val	GGG Gly	ACG Thr 155	ACC Thr	GAT Asp	CGG Arg	TTT Phe	GGT Gly 160	, 4	180
GTC Val	CCC Pro	ACG Thr	TAT Tyr	AAC Asn 165	TGG Trp	GGG Gly	GCG Ala	AAC Asn	GAC Asp 170	TCG Ser	GAT Asp	GTG Val	CTG Leu	ATT Ile 175	CTC Leu	3	528
AAC Asn	AAC Asn	ACG Thr	CGG Arg 180	CCG Pro	CCG Pro	CGA Arg	GGC Gly	AAC Asn 185	TGG Trp	TTC Phe	GGC Gly	TGT Cys	ACA Thr 190	TGG Trp	ATG Met	Ş	576

AAT Asn	GGC	ACT Thr 195	GGG Gly	TTC Phe	ACC Thr	AAG Lys	ACG Thr 200	TGT Cys	G G G Gly	GGC Gly	CCC Pro	CCG Pro 205	TGC Cys	AAC Asn	ATC Ile	624
GGG Gly	GGG Gly 210	GCC Ala	GGC Gly	AAC Asn	AAC Asn	ACC Thr 215	TTG Leu	ACC Thr	TGC Cys	CCC Pro	ACT Thr 220	GAC Asp	TGT Cys	TTT Phe	CGG Arg	672
AAG Lys 225	CAC His	CCC Pro	GAG Glu	GCC Ala	ACC Thr 230	TAC Tyr	GCC Ala	AGA Arg	TGC Cys	GGT Gly 235	TCT Ser	GGG Gly	CCC Pro	TGG Trp	CTG Leu 240	720
ACA Thr	CCT Pro	AGG Arg	TGT Cys	ATG Mec 245	GTT Val	CAT His	TAC Tyr	CCA Pro	TAT Tyr 250	AGG Arg	CTC Leu	TGG Trp	CAC His	TAC Tyr 255	CCC Pro	768
TGC Cys	ACT Thr	GTC Val	AAC Asn 260	TTC Phe	ACC Thr	ATC Ile	TTC Phe	AAG Lys 265	GTT Val	AGG Arg	ATG Met	TAC Tyr	GTG Val 270	GGG Gly	Gly GGC	816
GTG Val	GAG Glu	CAC His 275	AGG Arg	TTC Phe	GAA Glu	GCC Ala	GCA Ala 280	TGC Cys	AAT Asn	TGG Trp	ACT Thr	CGA Arg 285	GGA Gly	GAG Glu	CGT Arg	864
TGT Cys	GAC Asp 290	TTG Leu	GAG Glu	GAC Asp	AGG Arg	GAT Asp 295	AGA Arg	TCA Ser	GAG Glu	CTT Leu	AGC Ser 300	CCG Pro	CTG Leu	CTG Leu	CTG Leu	912
TCT Ser 305	ACA Thr	ACA Thr	GAG Glu	TGG Trp	CAG Gln 310	AGC	TTA Leu	ATT Ile	AAT Asn	TAG	300					945

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala 1 5 10 15

Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp 20 25 30

Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile 35 40 45

Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu 50 60

Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr 65 70 75 80

Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys

Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr 100 105 110

Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro 115 120 125

Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr 130 140

Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly 145 150 155 160

Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu 165 170 175

Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met 180 185 190

Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile 195 200 205

Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg 210 215 220

Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu 225 230 235 240

Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro 245 250 255

Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly 260 265 270

Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg
275 280 285

Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu 290 295 300

Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn 305

- (2) INFORMATION FOR SEQ ID NO: 43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 961 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..958
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide

(B) LOCATION: 1..955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

	(xi)	SEÇ	QUENC	E DE	ESCRI	PTIC)N: S	SEQ I	D NO	0: 43	3 :					
						AAG Lys										48
						CGC Arg										96
						CTC Leu										144
						GGC Gly 55										192
						CAA Gln										240
						TCT Ser										288
						GCT Ala										336
_						CAG Gln										384
CGA Arg	CCG Pro 130	TGT Cys	GGT Gly	ATT Ile	GTA Val	CCC Pro 135	GCG Ala	TCT Ser	CAG Gln	GTG Val	TGC Cys 140	GGT Gly	CCA Pro	GTG Val	TAT Tyr	432
						GTT Val										480
_						GGG Gly										528
						CGA Arg									ATG Met	576
AAT Asn	GGC Gly	ACT Thr 195	GGG Gly	TTC Phe	ACC Thr	AAG Lys	ACG Thr 200	TGT Cys	GGG Gly	GGC Gly	CCC Pro	CCG Pro 205	TGC Cys	AAC Asn	ATC Ile	624
															CGG Arg	672
AAG	CAC	CCC	GAG	GCC	ACC	TAC	GCC	AGA	TGC	GGT	TCT	GGG	CCC	TGG	CTG	720

Lys 225	His	Pro	Glu	Ala	Thr 230	Tyr	Ala	Arg	Cys	Gly 235	Ser	Gly	Pro	Trp	Leu 240	
					GTT Val											768
					ACC Thr	-	_	_	-						-	816
					GAA Glu						_				-	864
					AGG Arg											912
					CGA Arg 310										A	958
TAG																961

- (2) INFORMATION FOR SEQ ID NO: 44:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala 1 10 15

Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp 20 25 30

Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile 35 40 45

Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu 50 60

Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr 65 70 75 80

Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys 85 90 95

Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr 100 105 110

Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro 115 120 125

Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr

130 135 140 Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly 150 155 Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu 230 Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg 280 Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu 295 Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu

315

- (2) INFORMATION FOR SEQ ID NO: 45:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1395 base pairs
 - (B) TYPE: nucleic acid

310

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1392
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..1389
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Mec 1	Val	Ala	Gly	Ala 5	His	Trp	Gly	Val	Leu 10	Ala	Gly	Leu	Ala	Tyr 15	Tyr	
TCC Ser	ATG Met	GTG Val	GGG Gly 20	AAC Asn	TGG Trp	GCT Ala	AAG Lys	GTT Val 25	TTG Leu	GTT Val	GTG Val	ATG Met	CTA Leu 30	CTC Leu	TTT Phe	96
GCC Ala	GGC Gly	GTC Val 35	GAC Asp	GGG Gly	CAT His	ACC Thr	CGC Arg 40	GTG Val	TCA Ser	GGA Gly	GGG Gly	GCA Ala 45	GCA Ala	GCC Ala	TCC Ser	144
GAT Asp	ACC Thr 50	AGG Arg	GGC Gly	CTT Leu	GTG Val	TCC Ser 55	CTC Leu	TTT Phe	AGC Ser	CCC Pro	GGG Gly 60	TCG Ser	GCT Ala	CAG Gln	AAA Lys	192
ATC Ile 65	CAG Gln	CTC Leu	GTA Val	AAC Asn	ACC Thr 70	AAC Asn	GGC Gly	AGT Ser	TGG Trp	CAC His 75	ATC Ile	AAC Asn	AGG Arg	ACT Thr	GCC Ala 80	240
CTG Leu	AAC Asn	TGC Cys	AAC Asn	GAC Asp 85	TCC Ser	CTC Leu	CAA Gln	ACA Thr	GGG Gly 90	TTC Phe	TTT Phe	GCC Ala	GCA Ala	CTA Leu 95	TTC Phe	288
TAC Tyr	AAA Lys	CAC His	AAA Lys 100	TTC Phe	AAC Asn	TCG Ser	TCT Ser	GGA Gly 105	TGC Cys	CCA Pro	GAG Glu	CGC Arg	TTG Leu 110	GCC Ala	AGC Ser	336
TGT Cys	CGC Arg	TCC Ser 115	ATC Ile	GAC Asp	AAG Lys	TTC Phe	GCT Ala 120	CAG Gln	GGG Gly	TGG Trp	GGT Gly	CCC Pro 125	CTC Leu	ACT Thr	TAC Tyr	384
ACT Thr	GAG Glu 130	CCT Pro	AAC Asn	AGC Ser	TCG Ser	GAC Asp 135	CAG Gln	AGG Arg	CCC Pro	TAC Tyr	TGC Cys 140	TGG Trp	CAC His	TAC Tyr	GCG Ala	432
CCT Pro 145	CGA Arg	CCG Pro	TGT Cys	GGT Gly	ATT Ile 150	GTA Val	CCC Pro	GCG Ala	TCT Ser	CAG Gln 155	GTG Val	TGC Cys	GGT Gly	CCA Pro	GTG Val 160	480
TAT Tyr	TGC Cys	TTC Phe	ACC Thr	CCG Pro 165	AGC Ser	CCT Pro	GTT Val	GTG Val	GTG Val 170	GGG Gly	ACG Thr	ACC Thr	GAT Asp	CGG Arg 175	TTT Phe	528
GGT Gly	GTC Val	CCC Pro	ACG Thr 180	TAT Tyr	AAC Asn	TGG Trp	GGG Gly	GCG Ala 185	AAC Asn	GAC Asp	TCG Ser	GAT Asp	GTG Val 190	CTG Leu	ATT Ile	576
CTC Leu	AAC Asn	AAC Asn 195	ACG Thr	CGG Arg	CCG Pro	CCG Pro	CGA Arg 200	GGC Gly	AAC Asn	TGG Trp	TTC Phe	GGC Gly 205	TGT Cys	ACA Thr	TGG Trp	624
Met	AAT Asn 210	GGC Gly	ACT Thr	GGG Gly	TTC Phe	ACC Thr 215	AAG Lys	ACG Thr	TGT Cys	GGG Gly	GGC Gly 220	CCC Pro	CCG Pro	TGC Cys	AAC Asn	672
ATC Ile 225	GGG Gly	GGG Gly	GCC Ala	GGC Gly	AAC Asn 230	AAC Asn	ACC Thr	TTG Leu	ACC Thr	TGC Cys 235	CCC Pro	ACT Thr	GAC Asp	TGT Cys	TTT Phe 240	720
CGG Arg	AAG Lys	CAC His	CCC Pro	GAG Glu 245	GCC Ala	ACC Thr	TAC Tyr	GCC Ala	AGA Arg 250	TGC Cys	GGT Gly	TCT Ser	GGG Gly	CCC Pro 255	TGG Trp	768

CTG Leu	ACA Thr	CCT Pro	AGG Arg 260	TGT Cys	ATG Met	GTT Val	CAT His	TAC Tyr 265	CCA Pro	TAT Tyr	AGG Arg	CTC Leu	TGG Trp 270	CAC His	TAC Tyr	816
CCC Pro	TGC Cys	ACT Thr 275	GTC Val	AAC Asn	TTC Phe	ACC Thr	ATC Ile 280	TTC Phe	AAG Lys	GTT Val	AGG Arg	ATG Met 285	TAC Tyr	GTG Val	GGG Gly	864
GGC Gly	GTG Val 290	GAG Glu	CAC His	AGG Arg	TTC Phe	GAA Glu 295	GCC Ala	GCA Ala	TGC Cys	AAT Asn	TGG Trp 300	ACT Thr	CGA Arg	GGA Gly	GAG Glu	912
CGT Arg 305	TGT Cys	GAC Asp	TTG Leu	GAG Glu	GAC Asp 310	AGG Arg	GAT Asp	Arg Arg	TCA Ser	GAG Glu 315	CTT Leu	AGC Ser	CCG Pro	CTG Leu	CTG Leu 320	960
CTG Leu	TCT Ser	ACA Thr	ACA Thr	GAG Glu 325	TGG Trp	CAG Gln	ATA Ile	CTG Leu	CCC Pro 330	TGT Cys	TCC Ser	TTC Phe	ACC Thr	ACC Thr 335	CTG Leu	1008.
CCG Pro	GCC Ala	CTA Leu	TCC Ser 340	ACC Thr	GGC Gly	CTG Leu	ATC Ile	CAC His 345	CTC Leu	CAT His	CAG Gln	AAC Asn	ATC Ile 350	GTG Val	GAC Asp	1056
GTG Val	CAA Gln	TAC Tyr 355	CTG Leu	TAC Tyr	GGT Gly	GTA Val	GGG Gly 360	TCG Ser	GCG Ala	GTT Val	GTC Val	TCC Ser 365	CTT Leu	GTC Val	ATC Ile	1104
AAA Lys	TGG Trp 370	GAG Glu	TAT Tyr	GTC Val	CTG Leu	TTG Leu 375	CTC Leu	TTC Phe	CTT Leu	CTC Leu	CTG Leu 380	GCA Ala	GAC Asp	GCG Ala	CGC Arg	1152
ATC Ile 385	TGC Cys	GCC Ala	TGC Cys	TTA Leu	TGG Trp 390	ATG Met	ATG Mec	CTG Leu	CTG Leu	ATA Ile 395	GCT Ala	CAA Gln	GCT Ala	GAG Glu	GCC Ala 400	1200
GCC Ala	TTA Leu	GAG Glu	AAC Asn	CTG Leu 405	GTG Val	GTC Val	CTC Leu	AAT Asn	GCG Ala 410	GCG Ala	GCC Ala	GTG Val	GCC Ala	GGG Gly 415	GCG Ala	1248
CAT His	GGC Gly	ACT Thr	CTT Leu 420	TCC Ser	TTC Phe	CTT Leu	GTG Val	TTC Phe 425	TTC Phe	TGT Cys	GCT Ala	GCC Ala	TGG Trp 430	TAC Tyr	ATC Ile	1296
AAG Lys	GGC Gly	AGG Arg 435	CTG Leu	GTC Val	CCT Pro	GGT Gly	GCG Ala 440	GCA Ala	TAC Tyr	GCC Ala	TTC Phe	TAT Tyr 445	GGC Gly	GTG Val	TGG Trp	1344
CCG Pro	CTG Leu 450	CTC Leu	CTG Leu	CTT Leu	CTG Leu	CTG Leu 455	GCC Ala	TTA Leu	CCA Pro	CCA Pro	CGA Arg 460	GCT Ala	TAT Tyr	GCC Ala	TAGTAA	1395

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr 1 5 10 15

Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe 20 25 30 Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser

Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys 50 55 60

Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala 65 70 75 80

Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe 85 90 95

Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser 100 105 110

Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr 115 120 125

Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala 130 135 140

Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val 145 150 155 160

Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe 165 170 175

Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile 180 185 190

Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp 195 200 205

Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn 210 215 220

Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe 225 230 235 240

Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp 245 250 255

Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr 260 265 270

Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly 275 280 285

Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu 290 295 300

Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu 305 310 315 320

Leu	Ser	Thr	Thr	Glu	Trp	Gln	Ile	Leu	Pro	Cys	Ser	Phe	Thr	Thr	Leu
				325					330					335	

Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp 340 345 350

Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile 355 360 365

Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg 370 375 380

Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala 385 390 395 400

Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Val Ala Gly Ala 405 410 415

His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile 420 425 430

Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp 435 440 445

Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala 450 455 460

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2082 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..2079
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..2076
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu 1

48

96

GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
20 25 30

GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
ACA Thr	GGG Gly 50	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC ?he	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTG Leu	192
CTG Leu 65	TCC Ser	TGT Cys	CTG Leu	ACC Thr	GTT Val 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr 75	GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240
TCC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288
TAT Tyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
CTC Leu	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	ST0 CCC	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432
GTC Val 145	GAT Asp	TTG Leu	CTC Leu	GTT Val	GGG Gly 150	GCG Ala	GCT Ala	GCT Ala	TTC Phe	TGT Cys 155	TCC Ser	GCT Ala	ATG Met	TAC Tyr	GTG Val 160	480
GGG G1y	GAC Asp	CTC Leu	TGC Cys	GGA Gly 165	TCT Ser	GTC Val	TTC Phe	CTC Leu	GTC Val 170	TCC Ser	CAG Gln	CTG Leu	TTC Phe	ACC Thr 175	ATC Ile	528
TCG Ser	CCT Pro	CGC Arg	CGG Arg 180	CAT His	GAG Glu	ACG Thr	GTG Val	CAG Gln 185	GAC Asp	TGC Cys	AAT Asn	TGC Cys	TCA Ser 190	ATC Ile	TAT Tyr	576
Pro	Gly	CAC His 195	Ile	Thr	Gly	His	Arg 200	Met	Ala	Trp	Asp	Met 205	Met	Met	Asn	624
TGG Trp	TCG Ser 210	CCT Pro	ACA Thr	ACG Thr	GCC Ala	CTG Leu 215	GTG Val	GTA Val	TCG Ser	CAG G1n	CTG Leu 220	CTC Leu	CGG Arg	ATC Ile	CCA Pro	672
CAA Gln 225	GCT Ala	GTC Val	GTG Val	GAC Asp	ATG Met 230	GTG Val	GCG Ala	GGG Gly	GCC Ala	CAT His 235	TGG Trp	GGA Gly	GTC Val	CTG Leu	GCG Ala 240	720
GGC Gly	CTC Leu	GCC Ala	TAC Tyr	TAT Tyr 245	TCC Ser	ATG Met	GTG Val	GGG Gly	AAC Asn 250	TGG Trp	GCT Ala	AAG Lys	GTT Val	TTG Leu 255	GTT Val	768
Val	Met	CTA Leu	Leu 260	Phe	Ala	Gly	Val	Asp 265	Gly	His	Thr	Arg	Val 270	Ser	Gly	816
GGG Gly	GCA Ala	GCA Ala	GCC Ala	TCC Ser	GAT Asp	ACC Thr	AGG Arg	GGC Gly	CTT Leu	GTG Val	TCC Ser	CTC Leu	TTT Phe	AGC Ser	5ro CCC	864

275 280 285 GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC 912 Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His 290 295 ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC 960 Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe 310 315 TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA 1008 Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG 1056 Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp 345 GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC 1104 Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr 355 360 TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG 1152 Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln 370 GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG 1200 Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly 385 390 395 ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC 1248 Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp 410 TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG 1296 Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG 1344 Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly 435 440 GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys 450 CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC 1440 Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys 470 480 GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT 1488 Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT 1536 Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val 505 AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn 520 TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG 1632

T	rp	Thr 530	Arg	Gly	Glu	Arg	Cys 535	ąsk	Leu	Glu	ąz£	Arg 540	Asp	Arg	Ser	Glu	
L						CTG Leu 550											1680
						CCG Pro											1728
						GTG Val											1776
						AAA Lys							-				1824
						ATC Ile					-		_				1872
A					_	GCC Ala 630			_			-				GCG Ala 640	1920
						CAT His											1968
			-	_		_		-			_	-				GCC Ala	2016
												_				CCA Pro	2064
			TAT		TAG	TAA											2082

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 692 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu 1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala

		33					40					45			
Thr	Gly 50	Asn	Leu	Pro	Gly	Cys 55	Ser	Phe	Ser	Ile	Phe 60	Leu	Leu	Ala	Leu
Leu 65	Ser	Cys	Leu	Thr	Val 70	Pro	Ala	Ser	Ala	Tyr 75	Glu	Val	Arg	Asn	Va <u>l</u> 80
Ser	Gly	Met	Tyr	His 85	Val	Thr	Asn	Asp	90	Ser	Asn	Ser	Ser	Ile 95	Val
Tyr	Glu	Ala	Ala 100	Asp	Met	Ile	Met	His 105	Thr	Pro	Gly	Cys	Val 110	Pro	Cys
Val	Arg	Glu 115	Asn	Asn	Ser	Ser	Arg 120	Cys	GII	Val	Ala	Leu 125	Thr	Pro	Thr
Leu	Ala 130	Ala	Arg	Asn	Ala	Ser 135	Val	Pro	Ipr	Thr	Thr 140	Ile	Arg	Arg	His
Val 145	Asp	Leu	Leu	Val	Gly 150	Ala	Ala	Ala	?he	Cys 155	Ser	Ala	Met	Tyr	Val 160
Gly	Asp	Leu	Cys	Gly 165	Ser	Val	Phe	Leu	7al 170	Ser	Gln	Leu	Phe	Thr 175	Ile
Ser	Pro	Arg	Arg 180	His	Glu	Thr	Val	Gln 185	qzA	Cys	Asn	Cys	Ser 190	Ile	Tyr
Pro	Gly	His 195	Ile	Thr	Gly	His	Arg 200	Met	Ala	Trp	Asp	Met 205	Met	Met	Asn
Trp	Ser 210	Pro	Thr	Thr	Ala	Leu 215	Val	Val	Ser	Gln	Leu 220	Leu	Arg	Ile	Pro
Gln 225	Ala	Val	Val	Asp	Met 230	Val	Ala	Gly	Ala	His 235	Trp	Gly	Val	Leu	Ala 240
Gly	Leu	Ala	Tyr	Tyr 245	Ser	Met	Val	Gly	Asn 250	Trp	Ala	Lys	Val	Leu 255	Val
Val	Met	Leu	Leu 260	Phe	Ala	Gly	Val	Asp 265	GŢΫ	His	Thr	Arg	Val 270	Ser	Gly
Gly		Ala 275		Ser	qaA	Thr	Arg 280		Leu	Val	Ser	Leu 285		Ser	Pro
Gly	Ser 290	Ala	Gln	Lys	Ile	Gln 295	Leu	Val	Asn	Thr	Asn 300	Gly	Ser	Trp	His
Ile 305	Asn	Arg	Thr	Ala	Leu 310	Asn	Cys	Asn	çz£	Ser 315	Leu	Gln	Thr	Gly	Phe 320
Phe	Ala	Ala	Leu	Phe 325	Tyr	Lys	His	Lys	Phe 330	Asn	Ser	Ser	Gly	Cys 335	Pro
Glu	Arg	Leu	Ala 340	Ser	Cys	Arg	Ser	Ile 345	qz£	Lys	Phe	Ala	Gln 350	Gly	Trp
Gly	Pro	Leu 355	Thr	Tyr	Thr	Glu	Pro 360	Asn	Ser	Ser	Asp	Gln 365	Arg	Pro	Tyr
Cys	Trp	His	Tyr	Ala	Pro	Arg	Pro	Cys	Gly	Ile	Val	Pro	Ala	Ser	Gln

1

370 375 380 Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly 390 395 400 Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val 500 505 Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn 520/ Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu 535 Leu Ser Pro Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys 550 Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu 600 Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gin Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala 635 Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys 650 Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro 680

Arg Ala Tyr Ala 690

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..2430
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..2427
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

					AAA Lys											48
CGC Arg	CGC Arg	CCA Pro	CAG Gln 20	GAC Asp	GTC Val	AAG Lys	TTC Phe	CCG Pro 25	GGC Gly	GGT Gly	GGT Gly	CAG Gln	ATC Ile 30	GTT Val	GGT Gly	96
					CCG Pro											144
ACT Thr	AGG Arg 50	AAG Lys	ACT Thr	TCC Ser	GAG Glu	CGG Arg 55	TCG Ser	CAA Gln	CCT Pro	CGT Arg	GGG Gly 60	AGG Arg	CGA Arg	CAA Gln	CCT Pro	192
ATC Ile 65	CCC Pro	AAG Lys	GCT Ala	CGC Arg	CGA Arg 70	CCC Pro	GAG Glu	GGT Gly	AGG Arg	GCC Ala 75	TGG Trp	GCT Ala	CAG Gln	CCC Pro	GGG Gly 80	240
TAC Tyr	CCT Pro	TGG Trp	CCC Pro	CTC Leu 85	TAT Tyr	GGC Gly	AAT Asn	GAG Glu	GGC Gly 90	ATG Met	GGG Gly	TGG Trp	GCA Ala	GGA Gly 95	TGG Trp	288
					GGC Gly											336
CGG Arg	CGT Arg	AGG Arg 115	TCG Ser	CGT Arg	AAT Asn	TTG Leu	GGT Gly 120	AAG Lys	GTC Val	ATC Ile	GAT Asp	ACC Thr 125	CTT Leu	ACA Thr	TGĆ Cys	384
		GCC					TAC					GGC			CTA Leu	432
GGG	GGC	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAG	GAC	480

Gl 14	y Gly 5	Ala	Ala	Arg	Ala 150	Leu	Ala	His	Gly	Val 155	Arg	Val	Leu	Glu	Asp 160	
	C GTG y Val															528
	C CTC e Leu															576
	A GTG u Val															624
	C TCA n Ser 210	Ser														672
	G TGC Y Cys 5															720
	G CTC a Lev															768
	A ATA															816
	C GCT r Ala		Tyr													864
	G CTO n Leu 290	ı Phe														912
	T TGO n Cys 5															960
	T AT(p Met									_					_	1008
	G CT(1056
	G GGI		Leu					Tyr					Gly			1104
	T AA(a Ly: 37(s Val														1152
Tl	C CG Ar Ar					Ala					Thr					1200

					G1Y GGG											1248
					ATC Ile											1296
					TTT Phe											1344
					GAG Glu											1392
					GGT Gly 470											1440
					TGC Cys											1488
					GTG Val											1536
					ACG Thr											1584
					TCG Ser										CCG Pro	1632
					TTC Phe 550										TTC Phe 560	1680
															AAC Asn	1728
				Cys					Phe					Glu	GCC Ala	1776
			Arg					520					Arg		ATG Met	1824
		Tyr					Trp					Thr			TTC Phe	1872
	Ile					Met					. Val				TTC Phe 640	1920
GAA	GCC	GCA	TGC	TAA	TGG	ACT	CGA	GGA	GAG	CGI	TGT	GAC	TTG	GAG	G GAC	1968

Glu	Ala	Ala	Cys	Asn 645	Trp	Thr	Arg	Gly	Glu 650	Arg	Cys	Asp	Leu	Glu 655	Asp	
AGG Arg	GAT Asp	AGA Arg	TCA Ser 660	GAG Glu	CTT Leu	AGC Ser	CCG Pro	CTG Leu 665	CTG Leu	CTG Leu	TCT Ser	ACA Thr	ACA Thr 670	GAG Glu	TGG Trp	2016
CAG Gln	ATA Ile	CTG Leu 675	CCC Pro	TGT Cys	TCC Ser	TTC Phe	ACC Thr 680	ACC Thr	CTG Leu	CCG Pro	GCC Ala	CTA Leu 685	TCC Ser	ACC Thr	GGC Gly	2064
CTG Leu	ATC Ile 690	CAC His	CTC Leu	CAT His	CAG Gln	AAC Asn 695	ATC Ile	GTG Val	GAC Asp	GTG Val	CAA Gln 700	TAC Tyr	CTG Leu	TAC Tyr	GGT Gly	2112
GTA Val 705	GGG Gly	TCG Ser	GCG Ala	GTT Val	GTC Val 710	TCC Ser	CTT Leu	GTC Val	ATC Ile	AAA Lys 715	TGG Trp	GAG Glu	TAT Tyr	GTC Val	CTG Leu 720	2160
TTG Leu	CTC Leu	TTC Phe	CTT Leu	CTC Leu 725	CTG Leu	GCA Ala	GAC Asp	GCG Ala	CGC Arg 730	ATC Ile	TGC Cys	GCC Ala	TGC Cys	TTA Leu 735	TGG Trp	2208
ATG Met	ATG Met	CTG Leu	CTG Leu 740	ATA Ile	GCT Ala	CAA Gln	GCT Ala	GAG Glu 745	GCC Ala	GCC Ala	TTA Leu	GAG Glu	AAC Asn 750	CTG Leu	GTG Val	2256
GTC Val	CTC Leu	AAT Asn 755	GCG Ala	GCG Ala	GCC Ala	GTG Val	GCC Ala 760	GGG Gly	GCG Ala	CAT His	GGC Gly	ACT Thr 765	CTT Leu	TCC Ser	TTC Phe	2304
CTT Leu	GTG Val 770	TTC Phe	TTC Phe	TGT Cys	GCT Ala	GCC Ala 775	TGG Trp	TAC Tyr	ATC Ile	AAG Lys	GGC Gly 780	AGG Arg	CTG Leu	GTC Val	CCT Pro	2352
GGT Gly 785	GCG Ala	GCA Ala	TAC Tyr	GCC Ala	TTC Phe 790	TAT Tyr	GGC Gly	GTG Val	TGG Trp	CCG Pro 795	CTG Leu	CTC Leu	CTG Leu	CTT Leu	CTG Leu 800	2400
CTG Leu	GCC Ala	TTA Leu	CCA Pro	CCA Pro 805	CGA Arg	GCT Ala	TAT Tyr	GCC Ala	TAGT	TAA						2433

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 809 amino acids
 - (B) TYPE: amino acid(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly

Gly Val Tyr Leu Leu Pro Arg Gly Pro Arg Leu Gly Val Arg Ala

rnr	Arg 50	Lys	Thr	Ser	Glu	Arg 55	Ser	Gln	Pro	Arg	Gly 60	Arg	Arg	Gln	Pro
Ile 65	Pro	Lys	Ala	Arg	Arg 70	Pro	Glu	Gly	Arg	Ala 75	Trp	Ala	Gln	Pro	Gly 80
Tyr	Pro	Trp	Pro	Leu 85	TYT	Gly	Asn	Glu	Gly 90	Met	Gly	Trp	Ala	Gly 95	Zrp
Leu	Leu	Ser	Pro 100	Arg	Gly	Ser	Arg	Pro 105	Ser	Trp	Gly	Pro	Thr 110	qaƙ	3ro
Arg	Arg	Arg 115	Ser	Arg	Asn	Leu	Gly 120	Lys	Val	Ile	qzA	Thr 125	Leu	mhr	Cys
Gly	Phe 130	_	Asp	Leu	Val	Gly 135		Ile	Pro	Leu	Val 140		Ala	Pro	Leu
Gly 145	Gly	Ala	Ala	Arg	Ala 150	Leu	Ala	His	Gly	Val 155	Arg	Val	Leu	Glu	qeA 061
Gly	Val	Asn	Tyr	Ala 165	Thr	Gly	Asn	Leu	Pro 170	Gly	Cys	Ser	Phe	Se r 175	Ile
Phe	Leu	Leu	Ala 180	Leu	Leu	Ser	Cys	Leu 185	Thr	Val	Pro	Ala	Ser 190	Ala	Tyr
Glu	Val	Arg 195	Asn	Val	Ser	Gly	Met 200	Tyr	His	Val	Thr	Asn 205	gzA	Cys	Ser
Asn	Ser 210	Ser	Ile	Val	Tyr	Glu 215	Ala	Ala	Asp	Met	Ile 220	Met	His	Thr	Pro
Gly 225	Cys	Val	Pro	Cys	Val 230	Arg	Glu	Asn	Asn	Ser 235	Ser	Arg	Cys	Trp	7al 240
Ala	Leu	Thr	Pro	Thr 245	Leu	Ala	Ala	Arg	Asn 250	Ala	Ser	Val	Pro	Thr 255	Thr
Thr	Ile	Arg	Arg 260	His	Val	Asp	Leu	Leu 265	Val	Gly	Ala	Ala	Ala 270	Phe	Cys
Ser	Ala	Met 275	Tyr	Val	Gly	Asp	Leu 280	Cys	Gly	Ser	Val	Phe 285	Leu	Val	Ser
Gln	Leu 290	Phe	Thr	Ile	Ser	Pro 295	Arg	Arg	His	Glu	Thr 300	Val	Gln	Asp	Cys
Asn 305	Cys	Ser	Ile	Tyr	Pro 310	Gly	His	Ile	Thr	Gly 315	His	Arg	Met	Ala	Trp 320
Asp	Met	Met	Met	Asn 325	Trp	Ser	Pro	Thr	Thr 330	Ala	Leu	Val	Val	Ser 335	Gln
Leu	Leu	Arg	Ile 340	Pro	Gln	Ala	Val	Val 345	Asp	Met	Val	Ala	Gly 350	Ala	His
Trp	Gly	Val 355	Leu	Ala	Gly	Leu	Ala 360	Tyr	Tyr	Ser	Met	Val 365		Asn	Trp
Ala	Lvs	Val	Leu	Val	Val	Met	Leu	Leu	Phe	Ala	Glv	Val	Asp	G! v	His

	370					375					380				
Thr 385	Arg	Val	Ser	Gly	Gly 390	Ala	Ala	Ala	Ser	Asp 395	Thr	Arg	Gly	Leu	Val 400
Ser	Leu	Phe	Ser	Pro 405	Gly	Ser	Ala	Gln	Lys 410	Ile	Gln	Leu	Val	Asn 415	Thr
Asn	Gly	Ser	Trp 420	His	Ile	Asn	Arg	Thr 425	Ala	Leu	Asn	Cys	Asn 430	Asp	Ser
Leu	Gln	Thr 435	Gly	Phe	Phe	Ala	Ala 440	Leu	Phe	Tyr	Lys	His 445	Lys	Phe	Asn
Ser	Ser 450	Gly	Cys	Pro	Glu	Arg 455	Leu	Ala	Ser	Cys	Arg 460	Ser	Ile	Asp	Lys
Phe 465	Ala	Gln	Gly	Trp	Gly 470	Pro	Leu	Thr	Tyr	Thr 475	Glu	Pro	Asn	Ser	Ser 480
Asp	Gln	Arg	Pro	Tyr 485	Cys	Trp	His	Tyr	Ala 490	Pro	Arg	Pro	Cys	Gly 495	Ile
Val	Pro	Ala	Ser 500	Gln	Val	Cys	Gly	Pro 505	Val	Tyr	Cys	Phe	Thr 510	Pro	Ser
Pro	Val	Val 515	Val	Gly	Thr	Thr	Asp 520	Arg	Phe	Gly	Val	Pro 525	Thr	Tyr	Asn
	530		Asn			535					540				
545			Asn		550					555					560
			Cys	565					570					575	
			Thr 580					585					590		
		595	Arg				600					605			
	610		Pro			615					620				
625			Lys		630					635					640
			Cys	645					650					655	
			Ser 660					665					670		
		675	Pro				680					685			
ren	690	nls	Leu	HIS	GIN	Asn 695	ile	Val	Asp	Val	Gln 700	Tyr	Leu	Tyr	Gly

Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu 705 710 715 720

Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp
725 730 735

Met Met Leu Leu Ile Ala Gin Ala Glu Ala Ala Leu Glu Asn Leu Val740 745 750

Val Leu Asn Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe 755 760 765

Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro 770 780

Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu 200 785 790 795 800

Leu Ala Leu Pro Pro Arg Ala Tyr Ala 805

- (2) INFORMATION FOR SEQ ID NO: 51:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..17
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ser Asn Ser Ser Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys 1 5 10 15

Val

- (2) INFORMATION FOR SEQ ID NO: 52:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..22

THE PROPERTY OF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Gly Gly Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp

Ser Pro Thr Thr Ala Leu 20

- (2) INFORMATION FOR SEQ ID NO: 53:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..37
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr

Pro Gly Cys Gly Lys

- (2) INFORMATION FOR SEQ ID NO: 54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids

 - (B) TYPE: amino acid(C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..25
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:
 - Gly Gly Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr 10
 - Gln Leu Arg Arg His Ile Asp Leu Leu
- (2) INFORMATION FOR SEQ ID NO: 55:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..25
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Gly Gly Thr Pro Thr Leu Ala Ala Arg Asp Ala Ser Val Pro Thr Thr 10

Thr Ile Arg Arg His Val Asp Leu Leu

- (2) INFORMATION FOR SEQ ID NO: 56:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn 10

Ser Thr Gly Leu

- (2) INFORMATION FOR SEQ ID NO: 57:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp Cys Pro 10

Asn Ser Ser Ile

- (2) INFORMATION FOR SEQ ID NO: 58:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala His Asp Ala Ile 1 10 15

Leu His Thr Pro 20

- (2) INFORMATION FOR SEQ ID NO: 59:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr 1 10 15

Pro Gly Cys Val

- (2) INFORMATION FOR SEQ ID NO: 63:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

His Asp Ala Ile Leu His Thr Pro Gly Val Pro Cys Val Arg Glu Gly
1 5 10 15

Asn Val Ser

- (2) INFORMATION FOR SEQ ID NO: 61:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Cys Val Arg Glu Gly Asn Val Ser Arg Cys Trp Val Ala Met Thr Pro 1 $$ 5 $$ 10 $$ 15

Thr Val Ala Thr

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- (2) INFORMATION FOR SEQ ID NO: 62:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr 1 5 10 15

Gln Leu Arg Arg 20

- (2) INFORMATION FOR SEQ ID NO: 63:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser 1 5 10 15

Ala Thr Leu Cys 20

- (2) INFORMATION FOR SEQ ID NO: 64:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Leu Val Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu

10 15

Cys Gly Ser Val 20

- (2) INFORMATION FOR SEQ ID NO: 65:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Gly Cys $1 \hspace{1cm} 15$

Asn Cys Ser Ile 20

- (2) INFORMATION FOR SEQ ID NO: 66:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His 1 15

Arg Met Ala Trp 20

- (2) INFORMATION FOR SEQ ID NO: 67:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Thr Ala Ala Leu 20

- (2) INFORMATION FOR SEQ ID NO: 68:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Asn Trp Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile

Pro Gln Ala Ile 20

- (2) INFORMATION FOR SEQ ID NO: 69:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His

1 10 15

Trp Gly Val Leu 20

- (2) INFORMATION FOR SEQ ID NO: 70:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met
1 5 10 15

Val Gly Asn Met 20

- (2) INFORMATION FOR SEQ ID NO: 71:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala Glu Thr Ile Val Ser 1 5 10 15

Gly Gly Gln Ala 20

- (2) INFORMATION FOR SEQ ID NO: 72:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Ser Gly Leu Val Ser Leu Phe Thr Pro Gly Ala Lys Gln Asn Ile Gln 1 5 10 15

Leu Ile Asn Thr 20

- (2) INFORMATION FOR SEQ ID NO: 73:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Gln Asn Ile Gln Leu Ile Asn Thr Asn Gly Gln Trp His Ile Asn Ser 1 5 10 15

Thr Ala Leu Asn 20

- (2) INFORMATION FOR SEQ ID NO: 74:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Leu Asn Cys Asn Glu Ser Leu Asn Thr Gly Trp Trp Leu Ala Gly Leu 1 5 10 15

Ile Tyr Gln His Lys 20

- (2) INFORMATION FOR SEQ ID NO: 75:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ala Gly Leu Ile Tyr Gln His Lys Phe Asn Ser Ser Gly Cys Pro Glu 1 5 10 15

Arg Leu Ala Ser 20

- (2) INFORMATION FOR SEQ ID NO: 76:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp

15 10 Gln Gly Trp Gly (2) INFORMATION FOR SEQ ID NO: 77: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77: Thr Asp Phe Asp Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser Gly Pro Asp Gln 20 (2) INFORMATION FOR SEQ ID NO: 78: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78: Ala Asn Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro Pro Lys Pro Cys (2) INFORMATION FOR SEQ ID NO: 79: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79: Trp His Tyr Pro Pro Lys Pro Cys Gly Ile Val Pro Ala Lys Ser Val 10

Cys Gly Pro Val

20

- (2) INFORMATION FOR SEQ ID NO: 80:
 - (i) SEOUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Ala Lys Ser Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val 1 $$ 10 $$ 15

Val Val Gly Thr 20

- (2) INFORMATION FOR SEQ ID NO: 81:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly Ala Pro Thr 1 5 10 15

Tyr Ser Trp Gly 20

- (2) INFORMATION FOR SEQ ID NO: 82:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Gly Ala Pro Thr Tyr Ser Trp Gly Glu Asn Asp Thr Asp Val Phe Val 1 5 10 15

Leu Asn Asn Thr 20

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Ser Thr Gly Phe Thr Lys
1 10 15

Val Cys Gly Ala 20

- (2) INFORMATION FOR SEQ ID NO: 84:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Gly Phe Thr Lys Val Cys Gly Ala Pro Pro Val Cys Ile Gly Gly Ala 1 $$ 10 $$ 15

Gly Asn Asn Thr 20

- (2) INFORMATION FOR SEQ ID NO: 85:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Lys His Pro

- (2) INFORMATION FOR SEQ ID NO: 86:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Ser Arg Cys Gly

Ser Gly Pro Trp

- (2) INFORMATION FOR SEQ ID NO: 87:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro Arg Cys Leu Val Asp

Tyr Pro Tyr Arg

- (2) INFORMATION FOR SEQ ID NO: 88:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids

 - (B) TYPE: amino acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile

Asn Tyr Thr Ile

- (2) INFORMATION FOR SEQ ID NC: 89:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Pro Cys Thr Ile Asn Tyr Thr Ile Phe Lys Ile Arg Met Tyr Val Gly
1 5 10 15

Gly Val Glu His

- (2) INFORMATION FOR SEQ ID NO: 90:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Met Tyr Val Gly Gly Val Glu His Arg Leu Glu Ala Ala Cys As
n Trp 1 5 10 15

Thr Pro Gly Glu 20

- (2) INFORMATION FOR SEQ ID NO: 91:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid(C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Ala Cys Asn Trp Thr Pro Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp 1 10 15

Arg Ser Glu Leu 20

- (2) INFORMATION FOR SEQ ID NO: 92:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Thr Thr 1 5 10 15

Gln Trp Gln Val 20

- (2) INFORMATION FOR SEQ ID NO: 93:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Tyr Gln Val Arg Asn Ser Thr Gly Leu 1 5

- (2) INFORMATION FOR SEQ ID NO: 94:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: YES
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

ACGTCCGTAC GTTCGAATTA ATTAATCGA

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: YES

29

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:	
CCTCCGGACG TGCACTAGCT CCCGTCTGTG GTAGTGGTGG TAGTGATTAT CAATTAATTG	60
(2) INFORMATION FOR SEQ ID NO: 96: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:	
GTTTAACCAC TGCATGATG	19
(2) INFORMATION FOR SEQ ID NO: 97:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:	
GTCCCATCGA GTGCGGCTAC	20
(2) INFORMATION FOR SEQ ID NO: 98:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 45 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	

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(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 98:	
CGTGACAT	FGG TACATTCCGG ACACTTGGCG CACTTCATAA GCGGA	45
(2) INFO	DRMATION FOR SEQ ID NO: 99:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
	SEQUENCE DESCRIPTION: SEQ ID NO: 99:	
TGCCTCAT	AC ACAATGGAGC TCTGGGACGA GTCGTTCGTG AC	42
(2) INFO	RMATION FOR SEQ ID NO: 100:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 100:	
TACCCAGC	AG CGGGAGCTCT GTTGCTCCCG AACGCAGGGC AC	42
(2) INFO	RMATION FOR SEQ ID NO: 101:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 101:	
TGTCGTGGT	rg gggacggagg cctgcctagc tgcgagcgtg gg	42
(2) INFOR	RMATION FOR SEQ ID NO: 102:	
	SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 102:	
CGTTATGT	GG CCCGGGTAGA TTGAGCACTG GCAGTCCTGC ACCGTCTC	48
(2) INFO	RMATION FOR SEQ ID NO: 103:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 103:	
CAGGGCCG	TT CTAGGCCTCC ACTGCATCAT CATATCCCAA GC	42
(2) INFO	RMATION FOR SEQ ID NO: 104:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(vi \	SECTION OF DESCRIPTION, SECTION NO. 104.	
(YT)	SEQUENCE DESCRIPTION: SEQ ID NO: 104:	

CCGGAATGTA CCATGTCACG AACGAC

(2) INFORMATION FOR SEQ ID NO: 105:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105: GCTCCATTGT GTATGAGGCA GCGG	24
(2) INFORMATION FOR SEQ ID NO: 106:	44
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:	
GAGCTCCCGC TGCTGGGTAG CGC	23
(2) INFORMATION FOR SEQ ID NO: 107:	23
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:	
CCTCCGTCCC CACCACGACA ATACG	25
(2) INFORMATION FOR SEQ ID NO: 108:	~~

(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 108:	
CTACCCGG	GC CACATAACGG GTCACCG	27
(2) INFO	RMATION FOR SEQ ID NO: 109:	
	SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
	SEQUENCE DESCRIPTION: SEQ ID XX: 109: AC AACGGCCCTG GTGG	24
		44
	RMATION FOR SEQ ID NO: 110: SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
	SEQUENCE DESCRIPTION: SEQ ID NO: 110:	22
(2) INFO	RMATION FOR SEQ ID NO: 111:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid	

- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

GCCATACGCT CACAGCCGAT CCC

23

- (2) INFORMATION FOR SEQ ID NO: 112:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys

1 10 15

Ser Asn Ser Ser 20

- (2) INFORMATION FOR SEQ ID NO: 113:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp 1 5 10 15

Met Ile Met His Thr

20

- (2) INFORMATION FOR SEQ ID NO: 114:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val
1 5 10 15

Arg Glu Asn Asn Ser

- (2) INFORMATION FOR SEQ ID NO: 115:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu 1 5 10 15

Thr Pro Thr Leu Ala 20

- (2) INFORMATION FOR SEQ ID NO: 116:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro
1 5 10 15

Thr Thr Thr Ile Arg

- (2) INFORMATION FOR SEQ ID NO: 117:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117: Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu Leu Val 10 Gly Ala Ala Phe (2) INFORMATION FOR SEQ ID NO: 118: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118: Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly 10 Asp Leu Cys Gly Ser (2) INFORMATION FOR SEQ ID NO: 119: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119: Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro (2) INFORMATION FOR SEQ ID NO: 120: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val Gln 1 5 10 15

Asp Cys Asn Cys Ser 20

- (2) INFORMATION FOR SEQ ID NO: 121:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr 1 5 10 15

Gly His Arg Met Ala

- (2) INFORMATION FOR SEQ ID NO: 122:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp

1 5 10 15

Ser Pro Thr Thr Ala
20